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ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING HERPESVIRUSES

Abstract:

Antisense oligonucleotides are disclosed having a length of 15-30 nucleotides containing the CAT sequence and hybridizable to herpes simplex virus type I gene UL13, UL39, or UL40. These antisense oligomers inhibit the replication of the virus at least three-fold. Pharmaceutical compositions containing these oligonucleotides as the active ingredients are also disclosed.

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<b>(54) Title:</b> OLIGONUCLEOTIDE THERAPIES FOR MODULATING THE EFFECTS OF HERPESVIRUSES  <b>(57) Abstract</b> <p>Compositions and methods are provided for the treatment and diagnosis of herpesvirus infections. In accordance with preferred embodiments, oligonucleotides are provided which are specifically hybridizable with RNA or DNA deriving from a gene corresponding to one of the open reading frames UL5, UL8, UL9, UL13, UL29, UL30, UL39, UL40, UL42, and UL52 of herpes simplex virus type 1. The oligonucleotide comprises nucleotide units sufficient in identity and number to effect said specific hybridization. In other preferred embodiments, the oligonucleotides are specifically hybridizable with a translation initiation site; it is also preferred that they comprise the sequence CAT. Methods of treating animals suspected of being infected with herpesvirus comprising contacting the animal with an oligonucleotide specifically hybridizable with RNA or DNA deriving from one of the foregoing genes of the herpesvirus are disclosed. Methods for treatment of infections caused by herpes simplex virus type 1, herpes simplex virus type 2, cytomegalovirus, human herpes virus 6, Epstein Barr virus or varicella zoster virus are disclosed.</p>		

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**OLIGONUCLEOTIDE THERAPIES FOR  
MODULATING THE EFFECTS OF HERPESVIRUSES**

**FIELD OF THE INVENTION**

This invention relates to therapies and  
5 diagnostics for herpesvirus infections. In particular,  
this invention relates to antisense oligonucleotide  
interactions with certain portions of herpesvirus RNA which  
have been found to lead to modulation of the activity of  
the RNA and, thus, to modulation of the effects of the  
10 viruses themselves. This application is a continuation-  
in-part of U.S. Serial No. 485,297, filed February 26,  
1990.

**BACKGROUND OF THE INVENTION**

Approximately 500,000 new cases of genital herpes  
15 are reported each year, and it is estimated that 30 million  
Americans are affected by this currently incurable disease.  
Similarly, it is estimated that there is an annual  
incidence of 500,000 new cases of herpes simplex  
gingivostomatitis and at least 100 million Americans suffer  
20 from recurrent herpes labialis. Overall the prevalence of  
seropositive individuals in the general population is  
approximately 70-80%. Although recurrent herpes simplex  
virus infections are the most prevalent of all herpesvirus  
infections, there is a need to develop more specific forms  
25 of therapy for diseases such as herpes simplex



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encephalitis, keratoconjunctivitis, herpetic whitlow and disseminated herpes infections of neonates and immunocompromised hosts.

The incidence of encephalitis is low (one case in 250,000 individuals per year), yet with existing therapy, the mortality rate is as high as 40% and approximately 50% of the survivors are left with severe neurological sequelae. Ocular infections are neither rare nor trivial. They are usually caused by HSV-1 and are a leading cause of blindness in many countries of the world. Herpetic whitlow is an occupational hazard of nurses, dentists and physicians which begins with erythema and tenderness of the distal segments of the fingers and is followed by coalescence and enlargement of the vesicles. An accompanying lymphangitis and lymphadenopathy of the draining lymphatics is a common feature. Neonatal HSV infection is usually encountered as a consequence of a child being born through an infected birth canal. The incidence of the disease is approximately 1 in 10,000 births. Mortality in babies with limited infection can be as high as 20% while mortality of neonates from disseminated infection, even with current therapy, can approach 75% and many survivors have significant neurological impairment.

Currently, nucleoside analogs are clearly the preferred therapeutic agents for HSV infections. A number of pyrimidine deoxyribonucleoside compounds have a specific affinity for the virus-encoded thymidine (dCyd) kinase enzyme. The specificity of action of these compounds confines the phosphorylation and antiviral activity of these compounds to virus-infected cells. A number of drugs from this class, e.g., 5-iodo-dUrd (IDU), 5-trifluoromethyl-dUrd (FMAU), 5-ethyl-dUrd (EDU), (E)-5-(2-bromovinyl)-dUrd (BVDU), 5-iodo-dCyd (IDC), and 5-trifluoromethyl-dUrd (TFT), are either in clinical use or

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likely to become available for clinical use in the near future. IDU is a moderately effective topical antiviral agent when applied to HSV gingivostomatitis and ocular stromal keratitis, however, its use in controlled clinical studies of HSV encephalitis revealed a high toxicity associated with IDU treatment. Although the antiviral specificity of 5-arabinofuranosyl cytosine (Ara-C) was initially promising, its clinical history has paralleled that of IDU. The clinical appearance of HSV strains which are deficient in their ability to synthesize the viral thymidine kinase has generated further concern over the future efficacy of this class of compounds.

The utility of a number of viral targets has been defined for anti-HSV compound development. Studies with thiosemicarbazone compounds have demonstrated that inhibition of the viral ribonucleotide reductase enzyme is an effective means of inhibiting replication of HSV in vitro. Further, a number of purine nucleosides which interfere with viral DNA replication have been approved for treatment of human HSV infections. 9-( $\beta$ -D-arabinofuranosyl) adenine (Ara-A) has been used for treatment of HSV-1 keratitis, HSV-1 encephalitis and neonatal herpes infections. Reports of clinical efficacy are contradictory and a major disadvantage for practical use is the extremely poor solubility of Ara-A in water. 9-(2-hydroxyethoxymethyl) guanine (Acyclovir, ACV) is of major interest. In humans, ACV has been used successfully in the therapy of localized and disseminated HSV infections. However, there appear to be both the existence of drug-resistant viral mutants and negative results in double-blind studies of HSV-1 treatment with ACV. ACV, like Ara-A, is poorly soluble in water (0.2%) and this physical characteristic limits the application forms for ACV. The practical application of purine nucleoside analogs in an extended clinical situation suffers from

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their inherently efficient catabolism, which not only lowers the biological activity of the drug but also may result in the formation of toxic catabolites.

All of the effective anti-HSV compounds currently  
5 in use or clinical testing are nucleoside analogs. The efficacy of these compounds is diminished by their inherently poor solubility in aqueous solutions, rapid intracellular catabolism and high cellular toxicities. An  
10 additional caveat to the long-term use of any given nucleoside analog is the recent detection of clinical isolates of HSV which are resistant to inhibition by nucleoside compounds which were being administered in clinical trials. Antiviral oligonucleotides offer the  
15 potential of better compound solubilities, lower cellular toxicities and less sensitivity to nucleotide point mutations in the target gene than those typical of the nucleoside analogs.

It is apparent that new routes to the diagnosis and therapy of herpesvirus infections are greatly desired.  
20 It is particularly desired to provide compositions and methods for therapy which are, at once, highly effective and possessed of no or only minor side effects. Thus, the provision of antisense oligonucleotide therapies for herpesvirus infections in accordance with this invention  
25 satisfies the long-felt need for such therapies.

#### OBJECTS OF THE INVENTION

It is a principal object of the invention to provide therapies for herpesvirus and related infections.

It is a further object of the invention to  
30 provide antisense oligonucleotides which are capable of inhibiting the function of RNA of herpesviruses and related viruses.

Yet another object is to secure means for diagnosis of herpesvirus infection.

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These and other objects of this invention will become apparent from a review of the instant specification.

#### SUMMARY OF THE INVENTION

In accordance with the present invention,  
5 oligonucleotides and oligonucleotide analogs are provided which are specifically hybridizable with RNA or DNA deriving from a gene corresponding to one of the open reading frames UL5, UL8, UL9, UL13, UL29, UL30, UL39, UL40, UL42 AND UL52 of herpes simplex virus type 1. The  
10 oligonucleotide comprises nucleotide units sufficient in identity and number to effect such specific hybridization. It is preferred that the oligonucleotides or oligonucleotide analogs be specifically hybridizable with a translation initiation site and preferably that the  
15 oligonucleotide comprise a sequence CAT.

In accordance with preferred embodiments, the oligonucleotides and oligonucleotide analogs are designed to be specifically hybridizable with DNA or even more preferably, RNA from one of the species herpes simplex  
20 virus type 1 (HSV-1), herpes simplex virus type 2 (HSV-2), cytomegalovirus, human herpes virus 6, Epstein Barr virus (EBV) or varicella zoster virus (VZV). Such oligonucleotides and analogs are conveniently and desirably presented in a pharmaceutically acceptable carrier.

25 In accordance with other preferred embodiments, the oligonucleotides and oligonucleotide analogs are formulated such that at least some of the linking groups between nucleotide units of the oligonucleotide units comprise sulfur-containing species such as phosphorothioate  
30 moieties.

Other aspects of the invention are directed to methods for diagnostics and therapeutics of animals, especially humans, suspected of having a herpesvirus infection. Such methods comprise contacting either the  
35 animal or a body fluid of the animal with oligonucleotides

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or oligonucleotide analogs in accordance with the invention in order to inhibit the proliferation or effect of such infection, or to effect a diagnosis thereof.

Persons of ordinary skill in the art will  
5 recognize that the particular open reading frames described for herpes simplex virus type 1 find counterparts in the other viruses named. Thus each of herpes simplex virus type 2, cytomegalovirus, human herpes virus type 6, Epstein  
10 Barr virus and varicella zoster virus are believed to have many analogous open reading frames which code for proteins having similar functions. Accordingly, the present invention is directed to antisense oligonucleotide therapy where the oligonucleotides or oligonucleotide analogs are directed to any of the foregoing viruses, or indeed to any  
15 similar viruses which may become known hereafter, which have one or more of such analogous open reading frames. For convenience in connection with the present invention, all such viruses are denominated as herpesviruses.

#### BRIEF DESCRIPTION OF THE DRAWINGS

20 Figure 1 is a depiction of the arrangement of the genes of herpes simplex virus type 1 in accordance with the data of McGeoch, D.J. et. al.; J. Gen. Virol., 69, 1531-1574 (1988).

Figure 2A reflects certain open reading frames  
25 (ORFs) including the ORFs for UL39 (140,000d) and UL40 (40,000d) in herpes simplex virus type 1.

Figure 2B shows one of a nested set of five 3'-coterminial transcripts including the UL13 gene of HSV-1, strain 17.

30 Figure 3 depicts a comparison of the UL13 translational open reading frames (ORFs) of the HSV-1, strain 17 and HSV-2, strain HG52 mRNA species.

Figure 4 is a sequence comparison of the UL39 gene DNAs for HSV-1, strain 17 and HSV-2, strain 333 with

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the translation initiation codon highlighted at 238 of HSV-1.

Figure 5 is a sequence comparison of the UL40 gene DNAs for HSV-1, KOS strain and HSV-2, strain 333 with the translation initiation codon highlighted at 138 of HSV-1.

Figure 6 is tabulation of the homologous ORFS among HSV-1, VZV, and EBV as predicted from published DNA sequence data.

Figure 7 is a graphical depiction showing mean disease scores at various times after infection. Mice were infected with  $1 \times 10^5$  pfu of HSV-1 KOS and treatment was begun 4 hours pi. Each data point represents the mean disease scores of all mice in the group on the day indicated.

Figure 8 is a graphical depiction showing the effect of drug dose on disease scores. The mean disease scores are plotted v. the dose of ISIS 1082 for days 11, 13 and 15 post infection.

Figure 9 is a graphical depiction showing mean disease scores at various times after infection. Mice were infected with  $1 \times 10^5$  pfu of HSV-1, strain KOS, and treatment with ISIS 1082 was begun 4 hours pi. Each data point represents the mean disease scores of all mice in the group on a given day.

Figure 10 is a graph showing the effect of various ISIS oligonucleotides upon HSV infectious yield. HSV-1 (strain KOS) and HSV-2 (strain HG52) were used. The control yield of HSV in these experiments was  $8.1 \times 10^7$  pfu/ml and  $8.2 \times 10^7$  pfu/ml for HSV-1 and HSV-2, respectively.

Figure 11 is a photograph showing the effect of various oligonucleotides upon the *in vitro* translation of RNA. Numbers to the left of the gels indicate the relative molecular mass of marker proteins shown in Lane 1. The

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bold arrow points to the major polypeptide product synthesized from HSV RNAs. Lesser arrows point to the polypeptides synthesized from HSV RNA in the presence of inhibitory oligonucleotide. For translational inhibition, the molar ratio of oligonucleotide:RNA was 50:1. (A.) Specificity of oligonucleotide inhibitory effect. Lanes 2-10 contain *in vitro* translation products from reticulocyte lysates using the following: lane 2, no RNA; lanes 3-6, pIP-1 RNA (0.112 pmoles); lanes 7-10, 5L0 RNA (0.145 pmoles). Lanes 4 and 8, ISIS 1049; lanes 5 and 9, ISIS 1082; lanes 6 and 10, ISIS 1238. (B.) Spectrum of inhibitory activity. Lanes 2-8 contain *in vitro* translation products from reticulocyte lysates using the following: lane 2, no RNA; lanes 3-5, pIP-2 RNA (0.108 pmoles); lanes 6-8, pIP-1 RNA (0.112 pmoles); lanes 4 and 7, ISIS 1049; lanes 5 and 8, ISIS 1082.

Figure 12 depicts dose response curves showing inhibition of HSV-2 replication by treatment with various concentrations of ISIS oligonucleotides or Acyclovir. HSV-2 (strain HG52) was used in these infections. Control infections for the ACV-treated wells were adjusted in DMSO content to correspond to the level of DMSO present in cells treated with 1  $\mu$ M concentrations of ACV.

Figure 13 illustrates the dose-dependent inhibition of HSV-1 (strain KOS) by ISIS 1082, ACV or ISIS 1238 treatment. Error bars represent the standard deviation ( $p > .05$ ) of the mean value for each concentration of compound.

Figure 14 illustrates the dose-dependent inhibition of HSV-1 (strain F) by ISIS 1082, ACV or ISIS 1238 treatment. Error bars represent the standard deviation ( $p > .05$ ) of the mean value for each concentration of compound.

Figure 15 shows a dose dependent inhibition of HSV-1 strains by Acyclovir or ISIS 1082 treatment. Strains

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DM2.1 (Figure 15B) and PAAr<sup>5</sup> (PAAr5) (Figure 15A) were used. Control wells did not contain DMSO.

#### DETAILED DESCRIPTION OF THE INVENTION

Herpes simplex virus is the most studied of the human herpes viruses. The virus exists in two similar but distinct subtypes (HSV-1 and HSV-2); numerous strains of each subtype are known. Although the host range of some HSV strains is limited to certain tissues *in vivo*, the *in vitro* host range of all strains includes most human tissue types (both primary and transformed cells) as well as many non-human cells. The viral replication cycle is rapid, requiring approximately 24 hours for HSV-1 and 48 hours for HSV-2 to produce infectious progeny. The rapid replication and broad host range of HSV has resulted in an extensive molecular analysis of viral gene structure and of the control of viral gene expression during infection.

The productive infection of HSV consists of a number of differentiable stages which include: adsorption of the virus to the host cell membrane, fusion of the viral envelope with the cellular membrane, penetration of the non-enveloped virion to the nucleus of the cell, uncoating of viral nucleic acid, expression of viral genes and replication of the viral genome, nuclear packaging of the genome into newly formed viral capsids and finally, egress of the mature virion from the cell. Virally encoded proteins have been identified which control, in part, each of these stages of viral replication. The DNA sequence of the HSV-1 genome has been published and supports prior estimates that at least 71 unique viral proteins are encoded by the virus during a productive infection. McGeoch, D.J., Dolan, A., Donald, S., and Rixon, F.J. *J. Mol. Biol.* 181; 1-13 (1985); McGeoch, D.J., Dolan, A., Donald, S., and Brauer, D.H.K.; *Nucleic Acids Res.* 14: 1727-1745 (1986); McGeoch, D.J., Dalrymple, M.A., Davison, A.J., Dolan, A., Frame, M.C., McNab, D., Perry, L.J.,



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Scott, J.E., and Taylor, P.; *J. Gen. Virol.* 69: 1531-1574 (1988); and Perry, L.J. and McGeoch, D.J.; *J. Gen. Virol.* 69: 2831-2846 (1988).

The structure of HSV genes is quite simple. The transcription of each mRNA is controlled by a promoter region located immediately 5' to the mRNA cap site for that gene. Splicing of mRNAs is rare and restricted primarily to the immediate early class of transcripts. A unique mRNA species exists for each putative protein product encoded by the virus and each of the viral mRNAs are considered to act like a monocistronic species even though multiple open reading frames (ORFs) are present in many of the mRNAs. The control of viral gene expression is a finely orchestrated cascade which can be divided into three general stages: the immediate early, early and late phases. The immediate early transcripts are synthesized at the onset of viral replication, even in the presence of translational inhibitors such as cycloheximide. Thus, the synthesis of this class of transcripts is controlled by existing cellular proteins and/or proteins brought into the cell by the infecting virion. The immediate early proteins are known to influence cellular and viral gene expression in both positive and negative manners, and the expression of these proteins is important for the transcriptional activation of other HSV genes, especially the early genes. The early gene transcripts encode many of the viral products which are necessary for replication of the viral genome. Because the synthesis of late gene transcripts is controlled by both the immediate early proteins and template abundance, the late genes are transcribed maximally only after viral DNA synthesis. The proteins encoded by the late genes include the envelope glycoproteins, the capsid proteins and other proteins which are necessary to maintain viral structure or permit egress of newly formed virions from the cell.

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DNA sequence analysis predicts a conservative estimate of 71 proteins encoded within the HSV-1 genome. Figure 1 sets forth nomenclature of HSV-1 genes and genomic organization of the unique long (UL) and unique short (US) regions. Although a number of viral gene products have been shown to be dispensable to viral replication *in vitro*, only the viral thymidine kinase function has been known to be dispensable for viral growth in the human host. Logically, this leaves 70 gene targets which could be amenable to target-directed antiviral chemotherapy. During viral replication, the viral mRNAs represent the most diverse and versatile targets for antisense oligonucleotide inhibition.

Because the transcription of HSV mRNAs is tightly regulated within the cascade pattern of gene expression, the relative concentration of an HSV mRNA depends upon the time of sampling during the course of infection. Generally, maximal levels of mRNA concentration are reached at a time 3-4 hours after the onset of its synthesis. The rates of mRNA decay are not known for all of the HSV mRNAs; rates vary among the examples cited in the literature. A number of structural features of HSV mRNAs are important to the efficient translation of viral proteins. The 5' caps, consensus translation initiation codons and the 3' polyadenylated tails of HSV mRNAs are presumed to function in a manner analogous to similar mRNA structures which have been described for many cellular mRNAs. Splicing of HSV mRNAs is rare, but the splice sites of the immediate early transcripts represent another structural feature of the viral transcripts which could be considered as a feasible site of antisense inhibition. Additionally, unique structural features of the HSV UL48 mRNA have been reported to influence the rate of tegument protein synthesis. See Blair, E.D., Blair, C.C., and Wagner, E.K.; *J. Virol.* 61: 2499-2508 (1987). The presence of similar structures in

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other HSV mRNAs or the ability of these structures to influence synthesis of their cognate protein species has not been examined. Thus, a large number of potential structural regions of an HSV mRNA can be targeted as a putative site for antisense oligonucleotide inhibition of mRNA function. Indeed, the treatment of infected cells with oligonucleotides which are complementary to the splice sites of the US1 and US2 genes or the translation initiation region of the UL48 gene has resulted in the inhibition of HSV replication *in vitro*. See Smith, C.C., Aurelian, L., Reddy, M.P., Miller, P.S., and Ts'o, P.O.P.; *Proc. Natl. Acad. Sci. USA* 83: 2787-2792 (1986); and Ceruzzi, M, and Draper, K.; *Nucleosides and Nucleotides* 8: 815-818 (1989).

Viral gene products which are known to contribute a biological function to HSV replication can be categorized into three groups. These are 1. transcriptional activator or repressor proteins, 2. DNA replication proteins and 3. structural proteins. The immediate early class of HSV transcripts encode proteins which function as transcriptional activators and repressors of other viral genes. Strains of virus which are deficient in the production of these proteins have been reported and with the exception of the IE175 gene product, the immediate early proteins do not appear to be essential to viral replication. The transacting functions of other immediate early proteins can be substituted by either IE175 or host functions. The transcription of IE175 mRNA continues in the infected cell until levels of IE175 protein reach concentrations which inhibit the further transcription of IE175 mRNA. Thus, the inhibition of IE175 protein synthesis by an appropriate antisense oligonucleotide would result in steadily increasing levels of the IE175 mRNA, which could eventually exceed the molar threshold of concentration that represents the limit for effective

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oligonucleotide inhibition. An additional problem of antisense therapy designed for immediate early genes is that the temporal expression of the immediate early genes would necessitate a prophylactic administration of  
5 oligonucleotide for efficacy. Although this type of dosage is possible, it is not feasible in most human infections.

The most studied group of viral proteins are those involved in genomic replication. At least seven viral proteins (UL5, 8, 9, 29, 30, 42 and 52) are directly  
10 involved in viral DNA replication. The viral DNA polymerase, the thymidine kinase and the ribonucleotide reductase enzyme functions have been inhibited successfully with nucleoside analogs and work continues to find more potent versions of these compounds. The development of  
15 drug-resistant strains of HSV limit the feasibility of developing a nucleoside analog with long-term efficacy in clinical use. Because the transcription of some late viral genes depends upon gene dosage for efficient expression, antisense inhibition of viral structural protein synthesis  
20 could also be accomplished indirectly by targeting the DNA synthetic proteins.

The use of structural proteins in antiviral efforts has centered on the development of vaccines and represents an unexplored field for chemotherapeutic  
25 intervention with antisense compounds. Proteins classed into this group include those known to play roles in viral assembly and structural integrity, viral adsorption, virion fusion with the host cell membrane and virus penetration into the infected cell.

30 Recently it has been reported that some viral proteins may serve bifunctional roles in HSV replication. In accordance with the present invention, these are now believed to offer the opportunity to directly affect multiple levels of viral replication by inhibiting a single  
35 protein product. The members of this class of viral

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proteins (UL13 and UL39) are limited in number, but represent targets which are believed to be very promising candidates for antisense inhibition. The viral proteins identified as the UL13 and UL39 ORFs of HSV-1 exhibit a high degree of nucleotide sequence conservation among homologues of various HSV-1 and HSV-2 subtypes. The UL13 and UL39 genes have now been determined to be the best sites for targeting therapeutic attack. A third protein, UL40, which forms the active ribonucleotide reductase enzyme complex with the UL39 protein, is also now believed to be a promising target for antisense inhibition.

Additional proteins are also believed to be good targets for antisense oligonucleotide therapeutic attack. These include proteins from the open reading frames UL5, UL8, UL9, UL29, UL30, UL42 And UL52. Accordingly, the present invention is preferably directed to inhibition of the function of mRNAs deriving from a gene corresponding to one of the open reading frames UL5, UL8, UL9, UL13, UL29, UL30, UL39, UL40, UL42 AND UL52 of herpes simplex virus type 1.

The UL13 protein of HSV-1 is a virion capsid protein which putatively encodes a protein kinase activity that is responsible for the specific phosphorylation of virion capsid proteins. The protein is encoded by a 4.1 kb mRNA which is one of a nested set of five 3'-coterminally transcribed transcripts as depicted in Figure 2. The UL13 mRNA is a minor viral species which first appears at 3-4 hours after the onset of viral replication in tissue culture. The abundance of the UL13 mRNA increases somewhat after viral DNA replication occurs but remains low relative to the abundances of the major viral mRNAs throughout late times of infection. It has now been found through DNA sequence analysis that the mRNA sequence encoding UL13 is highly conserved among HSV-1 and HSV-2 isolates. The predicted molecular weights of the HSV-1 and HSV-2 proteins are 57193

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and 57001, respectively. Because the synthesis of UL13 protein is not detected until after the onset of viral DNA synthesis, it is assumed that the primary control of UL13 translation is the abundance of the 4.1 kb mRNA. The role, if any, of the 5' non-translated region of the 4.1 kb mRNA in controlling the rate of UL13 protein synthesis has not been examined. A comparison of the translational open reading frames (ORFs) of the HSV-1 and HSV-2 mRNA species depicted in Figure 3 reveals a conserved nucleotide sequence which is an attractive target for oligonucleotide inhibition of HSV UL13 synthesis and viral replication. The similarity in nucleotide sequence in this region (mismatches are only 205 of 1554 nucleotides) reflects an important structural feature of the mRNA which, it has now been found, can be exploited by antisense oligonucleotide therapy to achieve broad antisense inhibitory activity against both HSV-1 and HSV-2 with single oligonucleotide sequences.

The UL39 protein of HSV-1 is closely associated with a second protein which is encoded by a neighboring gene, UL40, to form a complex that exhibits a ribonucleotide reductase activity. See Frame, M.C., Marsden, H.S., and Dutia, B.M.; *J. Gen. Virol.* 66: 1581-1587 (1985). A homologous set of proteins is encoded by HSV-2 and exhibits a similar ribonucleotide reductase activity. Alone, the HSV-2 homolog of the UL39 protein possesses an autophosphorylating protein kinase activity. A similar kinase activity has not been demonstrated for the HSV-1 UL39 protein. The UL39 and UL40 proteins are encoded by a pair of 3' coterminal mRNAs which are 5.2 and 1.2 kb in length, respectively. In an HSV-1 infection, the 5.2 kb mRNA is a major mRNA early in infection that decreases in abundance at late times of infection. The 1.2 kb mRNA becomes modestly abundant at early times and remains so throughout the infection. In an HSV-2 infection, the 1.2

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kb mRNA homolog is the abundant early species and the 5.2 kb mRNA homolog is only moderately abundant. Again, both species of mRNA are only moderately abundant late in the infection. The biological significance of the differences in mRNA abundances between the HSV species is uncertain, but these differences may have profound effects upon the selection of an effective target for oligonucleotide inhibition of the viral ribonucleotide reductase or protein kinase activities. The proteins of the HSV ribonucleotide reductase complex are synthesized prior to viral DNA replication and the enzymatic activity probably plays an essential role in preparing substrates which are required for DNA synthesis. Inhibition of this important enzymatic function will not only interfere with DNA synthesis but also indirectly inhibit the synthesis of those late protein products whose encoding genes rely upon template abundance to efficiently synthesize the appropriate mRNAs. A comparison of the ORFs of the HSV ribonucleotide reductase mRNAs reveals a degree of nucleotide divergence, as shown in Figure 4, which may influence intertypic efficacy of the mRNA function. The divergence in nucleotide sequence around the AUG codons may require that separate nucleotide therapeutic preparations be used to inhibit the initiation of HSV-1 and HSV-2 UL39 and UL40 protein synthesis. Other regions within the body of the HSV-1 and HSV-2 UL39 and UL40 ORFs exhibit more extensive DNA homologies such that oligonucleotide preparations which have homologies to these regions may effectively inhibit replication of both HSV-1 and HSV-2.

The genome of HSV-1 contains both cis- and trans-acting elements which function in viral DNA replication. The cis-acting elements correspond to the origins of DNA replication and the trans-acting elements are the enzymes responsible for HSV-1 DNA replication. Seven of the open reading frames encoded by the HSV-1 genome correspond to

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the seven complementation groups known to be essential for HSV-1 DNA replication. These seven open reading frames encode the viral DNA polymerase enzyme (UL30), a single-stranded DNA binding protein (UL29), the ori<sub>L</sub>-binding protein (UL9), a double-stranded DNA binding protein (UL42), and three proteins which comprise the helicase-primase complex (UL5, UL8 and UL52). The DNA sequence of these genes is known only for the HSV-1 genome, but the general colinearity and gross DNA sequence homologies between the HSV-1 and HSV-2 genomes in regions encoding critical viral functions has been established such that it is likely that an oligonucleotide inhibitor for each of these HSV-1 gene functions will be found which will also inhibit functional expression of the homologous HSV-2 gene.

Three HSV gene targets have been reported to be sensitive to antisense inhibitors in *in vitro* assays. An oligonucleotide comprising a sequence of [dC]<sub>28</sub> linked internucleosidically by phosphorothioate groups inhibits HSV-2 DNA polymerase activity, but this action appears to be non-specific because the same oligonucleotide has also been shown to interfere with genomic replication of an unrelated virus, Human Immunodeficiency Virus. Cheng, Y-C., Gao, W., Stein, C.A., Cohen, J.S., Dutschman, G.E., and Hanes, R.N.; Abstract and poster presented at Oligonucleotides as Antisense Inhibitors of Gene Expression: Therapeutic Implications, held in Rockville, MD (1989); Matsukura, M., Shinozuka, K., Zon, G., Mitsuya, H., Reitz, M., Cohen, J.S., and Broder, S.; *Proc. Natl. Acad. Sci. USA* 84: 7706-7710 (1987). Although this oligonucleotide has been shown to inhibit the respective viral replicases, inhibition of viral replication is not realized. Methylphosphonate linked and psoralen-derivitized oligonucleotides complementary to the splice junction acceptor sites of the HSV-1 US1 and US12 mRNAs have been shown to inhibit HSV-1 replication *in vitro*.



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Kulka, M., Smith, C.C., Aurelian, L., Fischelevich, R., Meade, K., Miller, P., and T'so, P.O.P.; *Proc. Natl. Acad. Sci. USA* 86: 6868-6872 (1989); and Smith, C.C., Aurelian, L., Reddy, M.P., Miller, P.S., and Ts'o, P.O.P.; *Proc. Nat'l Acad. Sci, USA*, 83, 2787-2792 (1986). These results are intriguing because the target genes have been shown to be non-essential to HSV replication. An oligonucleotide sequence which is complementary to a gene which is essential to the replication of the virus is expected to be a better therapeutic agent than oligonucleotides targeted to non-essential gene products. Proof of this supposition was demonstrated by Ceruzzi and Draper using the HSV-1 UL48 mRNA as a target sequence. Ceruzzi, M, and Draper, K.; *Nucleosides and Nucleotides*, 8: 815-818 (1989). The antiviral efficacy achieved by Ceruzzi and Draper with a natural (phosphodiester-linked) oligonucleotide was reported to be comparable to the efficacy observed by Smith et. al. using their modified oligonucleotides. This increase in antiviral efficacy was probably related to the important role of the UL48 protein in enhancing immediate early transcription of the virus.

The development of a set of oligonucleotide inhibitors of the UL13 capsid protein synthesis and virion protein phosphorylation represents a novel target for anti-HSV chemotherapy. The targeting of a number of independent viral functions offers the opportunity for broad intertypic antiviral activity by using the most highly effective antisense oligonucleotides determined by our studies in combination with each other or with an existing nucleoside therapy. Comparison of the DNA sequences of herpes simplex virus type 1 (HSV-1), varicella zoster virus (VZV) and Epstein Barr Virus (EBV) has revealed that the genes which have now been found to be the best targets for antisense oligonucleotide attack are conserved among the human herpesviruses. The VZV and EBV genes which are homologous

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to the HSV-1 genes are set forth in Figure 6. The predictions of ORFs are taken from GenBank annotations of published DNA sequences. Davison, A.J. & Scott, J.E., *J. gen. Virol.* 67: 1759-1816 (1987); McGeoch, D.J., Dalrymple, M.A., Davison, A.J., Dolan, A., Frame, M.C., McNab, D., Perry, L.J., Scott, J.E., & Taylor, P., *J. Gen. Virol.* 69: 1531-1574 (1988); Baer, R., Bankier, A.T., Biggin, M.D., Deininger, P.L., Farrell, P.J., Gibson, T.J., Hatfull, G., Hudson, G.S., Satchwell, S.C., Sequin, C., Tuffnell, P.S., & Barrell, B.G., *Nature* 310: 207-211 (1984).

Although the EBV BBRF2 and BORF2 genes are listed as being homologous to HSV-1 UL9 and UL39 genes, respectively, the encoded amino acids of these genes are not highly homologous. This lack of amino acid homology in the encoded ORFs may reflect a disruption of the EBV ORFs by splicing events within the mRNAs although verification of splices within these mRNAs has not yet been made. A number of regions of nucleotide homology which exist within these various herpesvirus genes are now believed to be good targets for antisense oligonucleotide inhibition. It is believed that an oligonucleotide which inhibits HSV-1 and/or HSV-2 and also possesses homology to the corresponding nucleotide sequence of either VZV or EBV will be an effective inhibitor of VZV and/or EBV replication as well. The sequence of the other human herpesviruses has not been published *in toto*, but limited nucleotide data available has shown that Human Cytomegalovirus (HCMV) and Human Herpesvirus 6 (HHV 6) have homology to the HSV-1 UL13 gene. Lawrence, G.L., Chee, M., Craxton, M.A., Gompels, U.A., Honess, R.W., and Barrell, B.G.; *J. Virol.* 64: 287-299 (1989). Additionally, the DNA sequence of the HCMV homolog of the HSV-1 UL30 gene has been published (Kouzarides, T., Bankier, A.T., Satchwell, S.C., Weston, K., Tomlinson, P., and Barrell, B.G.; *J. Virol.* 61: 125-133 (1987) and shown to exhibit regions of homology to the

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HSV-1 gene. Once the sequences of other human herpesviruses are known, it is believed that the genes which have now been targeted will be retained at least in part and show significant nucleotide homology to the original HSV gene sequences. The present invention employs oligonucleotides and oligonucleotide analogs for use in antisense inhibition of the function of messenger RNAs of herpesviruses. In the context of this invention, the term "oligonucleotide" refers to a plurality of joined nucleotide units formed from naturally-occurring bases and cyclofuranosyl groups joined by native phosphodiester bonds. This term effectively refers to naturally-occurring species or synthetic species formed from naturally-occurring subunits.

"Oligonucleotide analog," as that term is used in connection with this invention, refers to moieties which function similarly to oligonucleotides but which have non naturally-occurring portions. Thus, oligonucleotide analogs may have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. They may also comprise altered base units or other modifications consistent with the spirit of this invention.

In accordance with certain preferred embodiments, at least some of the phosphodiester bonds of the oligonucleotide have been substituted with a structure which functions to enhance the ability of the compositions to penetrate into the region of cells where the RNA whose activity is to be modulated is located. It is preferred that such linkages be sulfur-containing. It is presently preferred that such substitutions comprise phosphorothioate bonds. Others such as alkyl phosphorothioate bonds, N-alkyl phosphoramidates, phosphorodithioates, alkyl phosphonates, and short chain alkyl or cycloalkyl

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structures may also be useful. In accordance with other preferred embodiments, the phosphodiester bonds are substituted with structures which are, at once, substantially non-ionic and non-chiral. Persons of  
5 ordinary skill in the art will be able to select other linkages for use in the practice of the invention.

Oligonucleotide analogs may also include species which include at least some modified base forms. Thus, purines and pyrimidines other than those normally found in  
10 nature may be so employed. Similarly, modifications on the cyclofuranose portions of the nucleotide subunits may also occur as long as the essential tenets of this invention are adhered to.

Such analogs are best described as being  
15 functionally interchangeable with natural oligonucleotides (or synthesized oligonucleotides along natural lines), but which have one or more differences from natural structure. All such analogs are comprehended by this invention so long as they function effectively to hybridize with messenger  
20 RNA of herpesvirus or related viruses to inhibit the function of that RNA.

The oligonucleotides and oligonucleotide analogs in accordance with this invention preferably comprise from about 6 to about 50 subunits. It is more preferred that  
25 such oligonucleotides and analogs comprise from about 8 to about 25 subunits. As will be appreciated, a subunit is a base and sugar combination suitably bound to adjacent subunits through phosphodiester or other bonds.

The oligonucleotides and oligonucleotide analogs  
30 of this invention are designed to be hybridizable with messenger RNA of herpesvirus. Such hybridization, when accomplished, interferes with the normal function of the messenger RNA to cause a loss of its utility to the virus. The functions of messenger RNA to be interfered with  
35 include all vital functions such as translocation of the

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RNA to the situs for protein translation, actual translation of protein from the RNA, and possibly even independent catalytic activity which may be engaged in by the RNA. The overall effect of such interference with the  
5 RNA function is to cause the herpesvirus to lose the benefit of the RNA and, overall, to experience interference with expression of the viral genome. Such interference is generally fatal to the virus.

In accordance with the present invention, it is  
10 preferred to provide oligonucleotides and oligonucleotide analogs designed to interfere with messenger RNAs determined to be of enhanced metabolic significance to the virus as described above. It has been found to be preferred to target one or more translation initiation  
15 portions of an open reading frame for antisense attack. As will be appreciated, such portions generally comprise the sequence AUG (in RNA) such that the oligonucleotide sequence CAT will be specifically hybridizable therewith. Accordingly, oligonucleotides and oligonucleotide analogs  
20 comprising the CAT sequence are preferred for these embodiments. Additional nucleotide subunits are preferably included in the oligonucleotide or oligonucleotide analog such that specific hybridization with the nucleic acid is attained to a high degree. Accordingly a number of  
25 subunits on one or either "side" of the CAT sequence which are designed to be complementary to the sequence adjacent to the translation initiation site to be hybridized with are included in the preferred oligonucleotides or analogs. Six to twelve subunits so adjacent on either "side" are  
30 convenient and are presently preferred, however larger or smaller numbers may be profitably employed without deviating from the spirit of this invention.

The oligonucleotides and oligonucleotide analogs of this invention can be used in diagnostics, therapeutics  
35 and as research reagents and kits. For therapeutic use,

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the oligonucleotide or oligonucleotide analog is administered to an animal, especially a human, suffering from a herpesvirus infection such as genital herpes, herpes simplex gingivostomatitis, herpes labialis, herpes simplex  
5 encephalitis, keratoconjunctivitis, herpetic whitlow or disseminated herpes infections of neonates and immunocompromised hosts.

It is generally preferred to apply the therapeutic agent in accordance with this invention  
10 topically or intralesionally. Other forms of administration, such as orally, transdermally, intravenously or intramuscularly may also be useful. Inclusion in suppositories may also be useful. Use of the oligonucleotides and oligonucleotide analogs of this  
15 invention in prophylaxis is also likely to be useful. Such may be accomplished, for example, by providing the medicament as a coating in gloves, condoms and the like. Use of pharmacologically acceptable carriers is also preferred for some embodiments.

20 The present invention is also useful in diagnostics and in research. Since the oligonucleotides and oligonucleotide analogs of this invention hybridize to herpesvirus, sandwich and other assays can easily be constructed to exploit this fact. Provision of means for  
25 detecting hybridization of oligonucleotide or analog with herpesvirus present in a sample suspected of containing it can routinely be accomplished. Such provision may include enzyme conjugation, radiolabelling or any other suitable detection systems. Kits for detecting the presence or  
30 absence of herpesvirus may also be prepared.

In accordance with the teachings of the invention, a number of complementary oligonucleotides which are targeted to the translation initiation regions of selected HSV mRNAs were made (Table 8). Natural  
35 oligonucleotides containing a phosphodiester backbone were

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screened for anti-HSV activity in an infectious yield assay. The oligonucleotide (ISIS 1049) which showed the best activity in this assay was targeted to an internal translation initiation codon of the HSV-2 homolog of the HSV-1 UL13 gene. Synthesis of methylphosphonate and phosphorothioate analogs of this active sequence showed that the phosphorothioate backbone modification greatly enhanced the antiviral activity of the oligonucleotide over that observed with either the phosphodiester or methylphosphonate oligonucleotides. Rabbit reticulocyte translation of *in vitro* synthesized HSV-1 and HSV-2 UL13 RNA demonstrated that oligonucleotides containing either a phosphodiester (ISIS 1049) or a phosphorothioate (ISIS 1082) backbone structure could inhibit the synthesis of the UL13 polypeptide. Dose response experiments compared the antiviral activity of ISIS 1082 with that of acycloguanosine (ACV) in two ACV<sup>r</sup> strains of HSV-1 PAAr<sup>5</sup>, a KOS mutant which has an altered nucleotide binding site in the viral DNA polymerase gene and DM2.1 which contains a deletion of the viral thymidine kinase gene. The activity of ISIS 1082 in these assays showed that the oligonucleotide does not require phosphorylation by the viral thymidine kinase for activation and indicated that the oligonucleotide does not interact with the viral DNA polymerase at the PAA and ACV binding site. *In vitro* assessment of the cellular toxicity of ISIS 1082 demonstrated that the predicted therapeutic index for the compound is equivalent to or better than that predicted for ACV in parallel assays. The demonstration that ISIS 1082 shows antiviral activity in ACV-resistant strains of virus and the favorable therapeutic index observed with the compound underscore the potential clinical value of this class of antiviral compounds.

Antisense oligonucleotides have been shown to inhibit the replication of virus in cell culture. Little

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is known, however, about the effectiveness of antisense oligonucleotides in animal models of viral infection. Animal models of HSV induced keratitis are well suited for such studies. Such ocular HSV infections are usually  
5 treated topically and thus provide a relatively simple way to test the effectiveness of antisense oligonucleotides *in vivo*. The drugs can be applied topically in aqueous solution and several parameters of the infection can be monitored. Using a murine model, the effectiveness of a  
10 phosphorothioate antisense oligonucleotide made in accordance with the teachings of the invention was tested for treatment of herpetic keratitis. The oligonucleotide was directed against the UL13 gene of HSV-1 having the sequence GCCGAGGTCCATGTCGTACGC (ISIS 1082; SEQ ID NO.: 7).  
15 It was found that topical treatment with this anti-UL13 oligonucleotide significantly reduced the severity of HSV induced stromal keratitis.

Three different concentrations of the oligonucleotide as well as a buffer control (50 mM sodium  
20 acetate, pH5.8, 0.15 M NaCl) and untreated animals infected with HSV-1 were tested. All animals were infected with  $1 \times 10^5$  plaque forming units (pfu) following scratching of the cornea. It was found that treatment with 0.3% and 1.0% ISIS 1082 did not affect the severity of blepharitis, but  
25 mice treated with 0.3% and 1.0% ISIS 1082 healed slightly faster (Figure 7). Treatment with ISIS 1082 reduced stromal disease and vascularization on days 11, 13, and 15 post-infection(Figure 7). This reduction in disease was statistically significant on some days but not on others,  
30 probably because of small sample size and variability in the disease. A comparison of dose vs disease scores as shown in Figure 8, indicated that ISIS 1082 has a narrow effective concentration range. The doses causing a 50% reduction in disease scores on day 15 post-infection were  
35 0.17%, 0.25%, and 0.22% for blepharitis, vascularization



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and stromal diseases, respectively. These results indicate that antisense oligonucleotides of the invention may be useful in treating HSV keratitis.

The invention is further illustrated by the following examples which are meant to be illustrations only and are not intended to limit the present invention to specific embodiments.

#### EXAMPLES

##### Example 1

10 HeLa (ATCC #CCL2) and Vero (ATCC #CCL81) cells used were obtained from the American Tissue Culture Collection. Cultures of HeLa cells were grown in Dulbecco's Modified Essential Medium (D-MEM) supplemented with 10% fetal bovine serum (FBS), penicillin (100  
15 units/ml), streptomycin (100 micrograms/ml), and L-glutamine (2mM). Cultures of Vero cells were grown in D-MEM supplemented with 5.0% FBS, penicillin, streptomycin and L-glutamine. Stock cultures of HSV-1 (strain KOS) and HSV-2 (strain HG52) were grown in Vero cells using low  
20 multiplicity infections (multiplicity of infection [MOI]=0.02 plaque forming units[pfu]/cell).

To assess the ability of oligonucleotides to inhibit HSV replication, an infectious yield assay was employed. HeLa cells were seeded at a density of  $5 \times 10^5$   
25 cells per well in Falcon 6 well tissue culture plates. Cells were overlaid with 3 ml of medium (D-MEM with 10% FBS) and incubated at 37°C for 18-24 hours. Where appropriate, cells were overlaid with oligonucleotide preparations in 1 ml of culture medium at 24 hours after  
30 seeding the plates. Following an 18 hours incubation, all wells were rinsed with phosphate buffered saline and infected with either HSV-1 or HSV-2 at varying multiplicities of infection (MOI) suspended in 0.5 ml of serum-free D-MEM. Virus and cells were incubated at 37°C

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for 1 hour with occasional rocking. Following viral adsorption, unadsorbed virus was rinsed away by washing the cells with phosphate buffered saline. Where appropriate, 1 ml of medium (D-MEM with 10% FBS) containing 4  $\mu$ M concentrations of oligonucleotide were added to the well and the cells were incubated for 48 hours at 37°C. Again, control wells received 1 ml of medium which contained no oligonucleotide.

The oligonucleotides used were designed to interfere with translation of either UL13, UL39 or UL40 mRNAs at a translation initiation region. Unmodified oligodeoxynucleotides were synthesized on an Applied Biosystems 380B DNA Synthesizer using standard phosphoramidite chemistry with oxidation by iodine. The reagents, both CPG-bound and  $\beta$ -cyanoethyldiisopropylphosphoramidites, were purchased from Applied Biosystems, Inc. (Foster City, CA). The standard oxidation bottle was replaced by 0.2 M solution of  $^3\text{H}$ -1,2-benzodithiole-3-one 1,1-dioxide (Iyer et al., (1990) *J. Am. Chem. Soc.*, 112, 1253-1254) in acetonitrile for the stepwise thiation of the phosphite linkages. The thiation cycle wait step was increased to 68 seconds and was followed by the capping step. After cleavage from the CPG-column and deblocking in concentrated ammonium hydroxide at 55°C (18 hours), the phosphorothioates were purified by trityl-on HPLC with a PRP-1 column using a gradient of acetonitrile in 50 mM of triethyl-ammonium acetate, pH 7 (4% to 32% in 30 minutes, flow rate of 1.5 ml/minute). Appropriate fractions were pooled, evaporated, and treated with 5.0% acetic acid at ambient temperature for 15 minutes. The solution was extracted with an equal volume of ethyl acetate, neutralized with ammonium hydroxide, frozen and lyophilized. Analytical gel electrophoresis was accomplished in 20% acrylamide, 8 M urea, 45 mM tris-borate buffer, pH 7, 40 V/cm. Oligodeoxynucleotides and their

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phosphorothioate analogs were judged from HPLC analysis and by polyacrylamide gel electrophoresis to be greater than 95% full length material.

The relative amounts of phosphorothioate and phosphodiester linkages obtained by our synthesis were determined by  $^{31}\text{P}$  NMR spectroscopy. The spectra were acquired on a Varian NMR spectrometer with a  $^{31}\text{P}$  frequency of 162 MHz. Typically, 1000 transients are co-added. A relaxation delay of 7.5 sec between transients is used to insure a fully relaxed spectrum. The  $^{31}\text{P}$  spectra are acquired at ambient temperature using deuterium oxide or dimethyl sulfoxide- $\text{d}_6$  as a solvent. Phosphorothioate samples typically contained less than one percent of phosphodiester linkages.

The sequences prepared are shown in Table 1.

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TABLE 1

GENE	HSV TYPE	OLIGONUCLEOTIDE SEQUENCE 5' 3'	(SEQ ID NO. :)	NORMAL STRUC. CODE #	PHOSPHO- THIOATE CODE #
5	UL48 1	GTC CGC GTC CAT GTC GGC	1	01	37
	UL13 1	GGA CTC ATC CAT CCT TCG GCC	2	02	34
	UL39 1	GCG GCT GGC CAT TTC AAC AGA	3	03	35
	UL40 1	CGC GGA ATC CAT GGC AGC AGG	4	04	36
	UL13 1	ACC GAG GTC CAT GTC GTA CGC	5	05	38
10	UL13 2	GGA CTC ATC CAT CCG TCC GCC	6	06	39
	UL13 2	GCC GAG GTC CAT GTC GTA CGC	7	07	40
	UL39 2	GCG GTT GGC CAT TGG AAC CAA	8	08	41

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Virus was harvested into the overlay medium and triplicate wells of each experimental point were combined and standardized to a volume of 3 ml. The suspension was frozen and thawed four times, then drawn through a 20 gauge  
5 needle four times and stored at -80°C in 2 ml aliquots. Alternatively, each well was harvested and prepared for replicate titrations at each experimental point. This latter protocol was used in the generation of dose response curves for individual strains of HSV-1. Virus titer was  
10 determined by plaque assay on Vero cell monolayers. Dilutions of each virus preparation were prepared and duplicate aliquots of each dilution were adsorbed onto Vero cells for 1 hour with occasional rocking. After adsorption, the virus inoculum was removed by rinsing the  
15 plates with phosphate buffered saline and the cells were overlaid with 2 ml of D-MEM containing 5.0% FBS and 0.75% methyl cellulose. Cells were incubated at 37°C for 72 hours before plaques were fixed with formalin, stained with crystal violet and counted. Plaque counts from treated  
20 wells were compared to those from the control wells to establish the degree of inhibition of virus replication.

Table 2 sets forth the data collected. The virus type, HSV-1 or HSV-2 and multiplicity of infection, MOI, are set forth. Inhibition of replication may be seen  
25 through comparison of experimental and control values.

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TABLE 2

	Virus Type	MOI	Oligo.	Yield 1	Yield 2	Average
5	HSV-1	0.5	none	5.4E+08	6.2E+08	5.80E+08
	HSV-1	0.5	01	6.3E+08	7.0E+08	6.65E+08
	HSV-1	0.5	03	7.7E+08	8.0E+08	7.85E+08
	HSV-1	0.5	04	3.9E+08	5.7E+08	4.80E+08
	HSV-1	0.5	05	7.7E+08	9.3E+08	8.50E+08
	HSV-1	0.5	08	7.9E+08	8.9E+08	8.40E+08
10	HSV-1	0.5	42	5.7E+07	7.5E+07	6.60E+07
	HSV-1	0.5	39	1.4E+06	1.7E+06	1.55E+06
	HSV-1	0.5	41	1.2E+06	2.6E+06	1.90E+06
15	HSV-2	0.5	none	8.0E+07	9.1E+07	8.55E+07
	HSV-2	0.5	01	7.6E+07	8.5E+07	8.05E+07
	HSV-2	0.5	03	8.3E+07	9.5E+07	8.90E+07
	HSV-2	0.5	04	4.9E+07	6.3E+07	5.60E+07
	HSV-2	0.5	05	6.6E+07	7.5E+07	7.05E+07
	HSV-2	0.5	08	5.1E+07	6.2E+07	5.65E+07
	HSV-2	0.5	39	5.0E+05	7.0E+05	6.00E+05
20	HSV-2	0.5	41	3.0E+05	7.0E+05	5.00E+05
	HSV-1	0.5	none	6.0E+07	7.6E+07	6.80E+07
	HSV-1	0.5	01	1.2E+08	1.2E+08	1.20E+08
	HSV-1	0.5	03	1.3E+08	1.7E+08	1.50E+08
	HSV-1	0.5	07	8.9E+07	9.5E+07	9.20E+07
	HSV-1	0.5	08	9.0E+07	1.2E+08	1.05E+08
	HSV-1	0.5	09	1.5E+08	1.8E+08	1.64E+08
	HSV-1	0.5	35	1.7E+07	2.0E+07	1.85E+07
	HSV-1	0.5	37	3.5E+07	4.7E+07	4.10E+07
25	HSV-1	0.5	38	5.7E+06	7.1E+06	6.40E+06
	HSV-1	0.5	40	1.7E+09	2.1E+09	1.86E+09
30	HSV-1	0.05	none	2.8E+08	3.3E+08	3.05E+08
	HSV-1	0.05	03	3.5E+08	4.7E+08	4.10E+08
	HSV-1	0.05	07	2.6E+08	3.2E+08	2.90E+08
	HSV-1	0.05	08	3.0E+08	4.3E+08	3.65E+08
	HSV-1	0.05	09	3.5E+08	3.7E+08	3.60E+08
	HSV-1	0.05	35	4.2E+05	6.0E+05	5.10E+05
35	HSV-1	0.05	37	2.9E+06	3.2E+06	3.05E+06
	HSV-1	0.05	38	2.5E+05	3.9E+05	3.20E+05
40	HSV-1	2.5	none	1.5E+08	2.5E+08	2.00E+08
	HSV-1	2.5	01	4.0E+08	7.1E+08	5.55E+08
	HSV-1	2.5	02	6.2E+08	7.6E+08	6.90E+08
	HSV-1	2.5	03	4.0E+08	4.3E+08	4.15E+08
	HSV-1	2.5	04	5.0E+08	6.1E+08	5.55E+08
	HSV-1	2.5	06	5.4E+08	6.1E+08	5.75E+08
	HSV-1	2.5	07	2.9E+08	4.1E+08	3.50E+08

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	HSV-1	0.25	none	7.7E+07	8.4E+07	8.05E+07
	HSV-1	0.25	01	6.5E+07	7.0E+07	6.75E+07
	Virus Type	MOI	Oligo.	Yield 1	Yield 2	Average
	HSV-1	0.25	02	5.9E+07	7.0E+07	6.45E+07
5	HSV-1	0.25	03	5.4E+07	6.4E+07	5.90E+07
	HSV-1	0.25	04	5.2E+07	7.1E+07	6.15E+07
	HSV-1	0.25	06	6.7E+07	7.2E+07	6.95E+07
	HSV-1	0.25	07	2.1E+07	4.3E+07	3.20E+07
	HSV-2	1.5	none	1.3E+08	1.7E+08	1.48E+08
10	HSV-2	1.5	01	5.9E+07	5.8E+07	5.85E+07
	HSV-2	1.5	02	5.3E+07	6.4E+07	5.85E+07
	HSV-2	1.5	03	1.1E+08	1.2E+08	1.15E+08
	HSV-2	1.5	04	1.3E+08	1.3E+08	1.28E+08
	HSV-2	1.5	06	1.1E+08	1.2E+08	1.12E+08
15	HSV-2	1.5	07	5.0E+07	5.4E+07	5.20E+07
	HSV-2	1.5	08	8.7E+07		8.70E+07
	HSV-2	0.15	none	8.0E+07	8.4E+07	8.20E+07
	HSV-2	0.15	01	2.8E+07	3.1E+07	2.95E+07
	HSV-2	0.15	02	7.3E+07	8.5E+07	7.90E+07
20	HSV-2	0.15	03	4.4E+07	5.0E+07	4.70E+07
	HSV-2	0.15	04	6.7E+07	7.2E+07	6.95E+07
	HSV-2	0.15	06	4.4E+07	4.8E+07	4.60E+07
	HSV-2	0.15	07	5.0E+07	5.4E+07	5.20E+07
	HSV-2	0.15	08	4.0E+07	4.1E+07	4.05E+07

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The following data were collected in a similar fashion except that the cells were pre-exposed to oligonucleotide for 5 hours rather than 18 hours. In some cases, as indicated, higher oligonucleotide concentrations were employed.

TABLE 3

	Virus Type	MOI	Oligo.	Yield 1	Yield 2	Average	
	HSV-1	0.5	none	6.1E+08	6.8E+08	6.45E+08	
	HSV-1	0.5	01	6.4E+08	7.4E+08	6.90E+08	
10	HSV-1	0.5	02	6.2E+08	6.5E+08	6.35E+08	8 $\mu$ M
	HSV-1	0.5	03	7.9E+08	9.0E+08	8.45E+08	11 $\mu$ M
	HSV-1	0.5	06	5.7E+08	7.0E+08	6.35E+08	
	HSV-1	0.5	07	7.0E+08	8.0E+08	7.50E+08	
	HSV-1	0.5	08	6.9E+08	8.9E+08	7.90E+08	15 $\mu$ M
15	HSV-1	0.5	09	6.6E+08	8.1E+08	7.35E+08	
	HSV-1	0.5	35	4.0E+05	5.0E+05	4.50E+05	
	HSV-1	0.5	37	1.8E+06		1.8E+06	
	HSV-1	0.5	38	3.2E+06	3.8E+06	3.50E+06	
	HSV-1	0.05	none	6.7E+08	8.6E+08	7.65E+08	
20	HSV-1	0.05	03	7.8E+07	9.0E+07	8.40E+07	11 $\mu$ M
	HSV-1	0.05	06	7.6E+07	7.7E+07	7.65E+07	
	HSV-1	0.05	07	8.4E+07	8.4E+07	8.40E+07	
	HSV-1	0.05	08	6.5E+07	8.3E+07	7.40E+07	15 $\mu$ M
	HSV-1	0.05	09	3.8E+07	4.5E+07	4.15E+07	
25	HSV-1	0.05	35	4.5E+04	4.8E+04	4.65E+04	
	HSV-1	0.05	37	9.5E+04	1.0E+05	9.95E+04	
	HSV-1	0.05	38	2.3E+04	2.7E+04	2.50E+04	
	HSV-2	0.5	none	5.3E+07	6.3E+07	5.80E+07	
	HSV-2	0.5	07	2.8E+07	3.0E+07	2.90E+07	
30	HSV-2	0.5	38	6.5E+06	7.1E+06	6.80E+06	
	HSV-2	0.05	none	4.3E+07	4.3E+07	4.30E+07	
	HSV-2	0.05	07	1.6E+07	1.8E+07	1.70E+07	
	HSV-2	0.05	38	6.7E+04	8.0E+04	7.35E+04	

From the foregoing, it is readily apparent that substantial reductions in virus replication can result from the application of oligonucleotides in accordance with this invention.



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Example 2

The following studies were designed to test the effectiveness of an antisense oligonucleotide complementary to the HSV-1 UL13 gene on ocular HSV infections in a murine model of HSV ocular disease.

Treatment Protocol

An anti-UL13 oligonucleotide, having the sequence GCCGAGGTCCATGTCGTACGC (ISIS 1082; SEQ ID NO.: 7), was dissolved in a buffer containing 50 mM sodium acetate (pH 5.8) and 0.15 M NaCl for administration to 4 to 5 week old female BALB/c mice. Three different doses of ISIS 1082 were tested and treatment was begun 4 hours post-infection (pi) with a laboratory strain of HSV-1 which causes severe ocular infections. The strain HSV-1 KOS (Grau et al., *Invest. Ophthalmol. Vis. Sci.*, 30:2474-2480 (1989) was used throughout these studies at an inoculum of  $1 \times 10^5$  plaque forming units (pfu).

To administer the test drug, mice were anesthetized with halothane (2.5%) inhalation. A 10  $\mu$ l drop of solution was placed on the cornea and the eye held open for 15 seconds. The mice were then returned to their cages. Excess drug was not removed. Treatment was administered every 2 hours for 16 hours per day (8 doses total per day) during the first 7 days and every 4 hours for 16 hours per day (4 doses per day) during the second week of treatment.

Mice were held for 30 days pi. At that time, trigeminal ganglia (TG) were aseptically removed. One half of the samples were homogenized, frozen and thawed 3 times and titered for infectious virus as described in Brandt and Grau, *Invest. Ophthalmol. Vis. Sci.*, 31:2214-2223 (1990). All samples were placed in 600  $\mu$ l of cell culture media prior to processing for the assay. Three mice were used

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for each group at each time point. Titers are reported as the mean total  $\log_{10}$  pfu per tissue.

The remaining samples were minced and placed in culture dishes containing monolayers of Vero cells in medium containing 2% serum. Co-cultures were monitored every other day for 2 weeks for evidence of cytopathic effect.

#### The Effect of Treatment on Ocular Disease

Three doses of ISIS 1082, buffer, and commercially available trifluorothymidine (TFT) solution (1.0%, Viroptic, Burroughs-Wellcome) were tested. The various treatment groups are listed in Table 4.

TABLE 4

	<u>Group</u>	<u>No. of Animals</u>	<u>Treatment</u>
15	A	10	Buffer Only
	B	10	0.1% ISIS 1082
	C	10	0.3% ISIS 1082
	D	9	1.0% ISIS 1082
	E	9	Viroptic (1.0%)
20	F	10	Mock Infected
	G	10	No Treatment

Figure 7 shows the results from scoring the mice for blepharitis, vascularization of the cornea, and stromal keratitis. Blepharitis was first visible on day 3 pi in groups A, B, C, D, and G, increased in severity, peaked on day 7, and then began to heal. The blepharitis scores on day 7 for groups A, B, C, D, and G were not significantly different ( $p > 0.05$ ) indicating that ISIS 1082 had little if any effect on the development of severe blepharitis. Blepharitis had healed completely by day 15 in groups C and D but took as long as 28 days in groups B and G, and did not heal completely in group D. The differences in disease

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scores between groups A, B, C, and D and G were significantly different on day 15 (  $p > 0.05$ ) indicating that treatment with ISIS 1082 reduced healing time. TFT (group E) prevented the development of significant  
5 blepharitis.

To determine if ISIS 1082 caused inflammation, 10 mice were mock infected with a 1.0% solution of ISIS 1082. The drug was given every 2 hours (8 doses per day) for 7 days and blepharitis was scored daily. None of the mice  
10 developed any signs of blepharitis or inflammation. Therefore, the blepharitis seen in ISIS 1082 treated animal (Figure 7) was not caused by the drug.

Vascularization of the cornea was first detected between days 5 and 7 and increased in severity in groups A,  
15 B, C, D, and G. Vascularization peaked on day 11 in untreated, infected mice (group G), declined slightly on day 13, but remained high even out to day 28 pi (score 1.2). Vascularization peaked on day 13 (score 1.7) and remained high in mice treated with buffer only. Mice  
20 treated with ISIS 1082 developed vascularization that peaked on day 13 and then remained constant out to day 28 pi regardless of the dose. However, the vascularization in the ISIS 1082 treated groups was less severe than untreated or buffer treated mice (scores of 0.8 to 1.2 vs 1.7,  
25 respectively, on day 13), indicating that although ISIS 1082 did not prevent vascularization, it did reduce the severity of the disease. A mild vascularization was observed on day 15 in mice treated with TFT (group F) but cleared quickly.

30 Mice in groups A, B, C, D, and G all developed stromal keratitis. Stromal keratitis was first detected on days 7 and 8, increased in severity, and peaked between days 11 and 15 in groups A and G. Stromal keratitis did not peak until day 15 or 21 in mice treated with ISIS 1082  
35 and was less severe on days 11, 13, and 15 compared to

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untreated and buffer treated mice. Mice treated with TFT developed mild stromal keratitis on day 15 that cleared by day 21.

The time course data for days 11, 13, and 15 were analyzed for statistically significant differences by ANOVA at the 95%, 90%, and 85% confidence levels. The results are shown in Table 5.

TABLE 5

Stromal Keratitis

Day 11							
	A	B	C	D	E	F	G
A	-	0	+	+	*	*	0
B		-	0	0	*	*	+
C			-	0	#	#	*
D				-	#	+	*
E					-	0	*
F						-	*
G							-

Day 13							
	A	B	C	D	E	F	G
A	-	0	+	0	*	*	0
B		-	0	0	*	*	0
C			-	0	0	0	*
D				-	0	#	*
E					-	0	*
F						-	*
G							-

Day 15							
	A	B	C	D	E	F	G
A	-	0	*	0	*	*	0
B		-	#	0	*	*	0
C			-	0	0	0	*
D				-	+	*	0
E					-	0	*
F						-	*
G							-

Vascularization

Day 11							
	A	B	C	D	E	F	G
A	-	0	0	0	*	*	0
B		-	0	0	*	*	+
C			-	0	*	*	0
D				-	*	*	0
E					-	0	*
F						-	*
G							-

Day 13							
	A	B	C	D	E	F	G
A	-	0	+	#	*	*	0
B		-	0	#	*	*	0
C			-	0	#	+	*
D				-	+	*	+
E					-	0	*
F						-	*
G							-

Day 15							
	A	B	C	D	E	F	G
A	-	0	*	0	*	*	0
B		-	0	0	*	*	0
C			-	0	0	#	*
D				-	#	*	0
E					-	0	*
F						-	*
G							-

Blepharitis

Day 11							
	A	B	C	D	E	F	G
A	-	0	0	0	*	*	0
B		-	0	0	#	+	0
C			-	0	0	0	+
D				-	+	*	0
E					-	0	*
F						-	*
G							-

Day 13							
	A	B	C	D	E	F	G
A	-	0	#	+	*	*	0
B		-	0	0	+	*	0
C			-	0	0	0	#
D				-	0	0	+
E					-	0	*
F						-	*
G							-

Day 15							
	A	B	C	D	E	F	G
A	-	0	*	*	*	*	0
B		-	*	*	*	*	0
C			-	0	0	0	+
D				-	0	0	#
E					-	0	#
F						-	+
G							-

\* = 95% confidence  
 + = 90% confidence  
 # = 85% confidence

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This analysis shows that 0.3% and 1.0% ISIS 1082 solutions significantly reduced the severity of stromal keratitis and vascularization of the cornea on days 11, 13, and 15 compared to the untreated and buffer treated mice. In some instances, a disease score will be significantly different on one day but not on another. It was also found that groups that should have been significantly different were not. For example, stromal keratitis scores for 0.3% ISIS 1082 treated mice were significantly different from buffer treated mice on day 15 but the 1.0% ISIS 1082 treated mice were not significantly different even though the two groups have similar disease scores. These difficulties in statistical interpretation of the data are caused by variability in disease scores, which is normal in these types of studies, and the sample size.

#### The Effect of Treatment on In Vivo Replication

10 Mice were infected with  $1 \times 10^5$  pfu of HSV-1 KOS and on days 1, 2, 3, 6, 8, and 10 post-infection, the eyes, TG, and eyelids were removed and the amount of infectious virus measured, as described above. The results are shown in Table 6.

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TABLE 6

Eye Titers<sup>+</sup>

Group	Treatment	Day				
		1	2	3	6	8 10
5	A Buffer	4.36(3/3)*	4.47(3/3)	2.45(3/3)	2.65(3/3)	0(0/3) 0(0/2)
	B 0.1% IS-1082	4.13(3/3)	3.04(3/3)	3.94(2.3)	2.58(2/3)	1.98(2/2) 0(0/2)
	C 0.3% IS-1082	4.38(3/3)	4.27(1/3)	3.37(3/3)	2.48(2/3)	0(0/3) 0(0/2)
	D 1.0% IS-1082	3.36(2/2)	4.19(3/3)	2.43(1/2)	3.11(2/3)	2.59(1/2) 0(0/2)
	E 1.0% TFT	3.04(3/3)	2.98(2/3)	0(0/3)	0(/3)	0(0/3) 0(0/2)
	G None	4.06(3/3)	4.27(3/3)	3.64(2/3)	2.60(3/3)	0(0/3) 0(0/2)
10	A Buffer	4.36(3/3)*	4.47(3/3)	2.45(3/3)	2.65(3/3)	0(0/3) 0(0/2)
	B 0.1% IS-1082	4.13(3/3)	3.04(3/3)	3.94(2.3)	2.58(2/3)	1.98(2/2) 0(0/2)
	C 0.3% IS-1082	4.38(3/3)	4.27(1/3)	3.37(3/3)	2.48(2/3)	0(0/3) 0(0/2)
	D 1.0% IS-1082	3.36(2/2)	4.19(3/3)	2.43(1/2)	3.11(2/3)	2.59(1/2) 0(0/2)
	E 1.0% TFT	3.04(3/3)	2.98(2/3)	0(0/3)	0(/3)	0(0/3) 0(0/2)
	G None	4.06(3/3)	4.27(3/3)	3.64(2/3)	2.60(3/3)	0(0/3) 0(0/2)

Eyelid Titers<sup>+</sup>

15	A Buffer	2.71(1/3)	2.06(1/3)	3.56(1/3)	1.96(2/3)	2.16(1/3) 0(0/2)
	B 0.1% IS-1082	0(0/3)	0(0/3)	1.83(1/3)	0(0/3)	0.78(1/3) 0(0/2)
	C 0.3% IS-1082	0(0/3)	0(0/3)	3.92(2/2)	3.42(2/3)	2.20(2/3) 0(0/2)
	D 1.0% IS-1082	0(0/3)	2.13(2/3)	3.45(1/3)	2.70(1/3)	0(0/2) 0(0/2)
	E 1.0% TFT	0(0/3)	0(0/3)	0(0/2)	0(0/3)	0(0/2) 0(0/2)
	G None	0(0/3)	2.43(1/2)	0.78(1/2)	0.60(1/3)	0(0/2) 0(0/2)
20	A Buffer	2.71(1/3)	2.06(1/3)	3.56(1/3)	1.96(2/3)	2.16(1/3) 0(0/2)
	B 0.1% IS-1082	0(0/3)	0(0/3)	1.83(1/3)	0(0/3)	0.78(1/3) 0(0/2)
	C 0.3% IS-1082	0(0/3)	0(0/3)	3.92(2/2)	3.42(2/3)	2.20(2/3) 0(0/2)
	D 1.0% IS-1082	0(0/3)	2.13(2/3)	3.45(1/3)	2.70(1/3)	0(0/2) 0(0/2)
	E 1.0% TFT	0(0/3)	0(0/3)	0(0/2)	0(0/3)	0(0/2) 0(0/2)
	G None	0(0/3)	2.43(1/2)	0.78(1/2)	0.60(1/3)	0(0/2) 0(0/2)

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## Trigeminal Ganglia Titers\*

5	A	Buffer	0(0/3)	0(0/2)	2.18(2/2)	3.71(3/3)	1.75(2/3)	0(0/1)
	B	0.1% IS-1082	0(0/3)	0(0/3)	0(0/3)	3.29(3/3)	2.66(3/3)	0(0/2)
	C	0.3% IS-1082	0(0/3)	0(0/3)	3.26(1/2)	0.30(1/3)	2.32(2/3)	0(0/2)
	D	1.0% IS-1082	0(0/3)	0(0/3)	0(0/3)	2.88(2/3)	0(0/2)	0(0/2)
	E	1.0% TFT	0(0/3)	0(0/3)	0(0/3)	0.30(1/3)	0(0/3)	0(0/2)
	G	None	0(0/3)	0(0/3)	2.58(1/3)	3.89(3/3)	2.78(2/3)	0(0/2)

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\* Log<sub>10</sub> of mean total pfu for 3 mice per day

\* No. positive/no. tested

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Dose Response to ISIS 1082

The results presented in Figure 7 indicate that there was some effect of drug dose on ocular disease. Figure 8 shows drug dose vs disease scores for blepharitis, vascularization, and stromal keratitis on days 11, 13, and 15 pi. In general, disease severity decreased at doses of 0.3% and 1.0% ISIS 1082. The high dose of ISIS 1082 (1.0%) did not appear to be more effective than the lower dose (0.3%). The antiviral effect of a 5.0% solution of ISIS 1082 compared to the lower concentrations versus HSV-1, strain KOS, in the murine ocular model of stromal keratitis is summarized in Figure 9. As shown, treatment with a 5.0% solution of ISIS 1082 gave significant improvement in mean disease scores of stromal keratitis at day 11 pi. The reduction in disease with a 5.0% solution was greater than the reduction with a 0.3% solution, which in turn was greater than the reduction with a 0.1% solution. These dose dependent efficacy curves are similar to the effects observed in earlier experiments, which were summarized in Figures 7 and 8.

Establishment of Latency

The effect of drug treatments on latency was also determined. TG were removed at 28 days pi. One half of the tissues were assayed directly for infectious virus and the remaining samples were assayed by co-cultivation on Vero cells for reactivatable latent infection. None of the tissues were positive when titrated directly for virus. As shown in Table 7, none of the TG from mice treated with 1.0% TFT were positive for reactivatable virus. Reactivatable virus was detected in TG from mice in all other treatment groups. By day 14 of co-



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cultivation, between 60 and 100% of the samples were positive.

TABLE 7

5	Group	Virus	Treatment	Reactivation	
				Day 7	Day 14
	A	+	Buffer	3/5‡ (60) §	3/5 (60)
	C	+	0.3% IS-1082	3/5 (60)	5/5 (100)
10	D	+	1.0% IS-1082	3/5 (60)	4/5 (80)
	E	+	TFT	0/5 (0)	0/5 (0)
	F	-	None	ND* -	ND* -
	G	+	None	3/5 (60)	4/5 (80)

Days after establishment of co-cultures

15 ‡No. positive/no. tested

\*Not done

§% of samples positive

### Example 3

#### Effect of Various Oligonucleotides Upon HSV Yield

20 The effect of various oligonucleotides upon the replication of HSV was examined using an infectious yield assay, as generally described in Example 1.

HSV-1 strains PAAr<sup>5</sup> and DM.2.1 were obtained from Burroughs Wellcome Company.

25 Plasmids used for the *in vitro* synthesis of HSV-1 and HSV-2 UL13 RNAs were constructed by cloning relevant pieces of the HSV genes into the KpnI and BamHI restriction endonuclease sites in the polylinker region of the transcription vector pSP72 (Promega Corporation).

30 The insertion in plasmid pIP-1 consists of a 3245 nucleotide KpnI-BglIII fragment of HSV-1 DNA which was

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taken from plasmid p1B01 (kindly supplied by S. Weller, University of Connecticut Health Center, Farmington, CN) containing the HSV-1 BglIII fragment 0 DNA. The KpnI-BglIII fragment contains coding sequences which begin  
5 at nucleotide +68 within the 5', nontranslated portion of the HSV-1 UL13 mRNA, traverse the entire open reading frame encoding the UL13 protein and end at nucleotide +3313 within the UL13 mRNA. The insertion in plasmid pIP-2 consists of a 1684 nucleotide KpnI-Bam HI fragment  
10 of HSV-2 DNA which was taken from plasmid BEDJ (kindly supplied by E. Wagner, University of California, Irvine, CA) containing the coding region of the HSV-2 homolog to the UL13 gene. The KpnI-BamHI fragment contains coding sequences which begin at nucleotide +68 within the 5',  
15 nontranslated portion of the HSV-2 mRNA, traverse through the entire open reading frame encoding the UL13 protein and end at nucleotide +1752 within the UL13 mRNA. The HSV DNA inserts in plasmids pIP-1 and pIP-2 are oriented so that transcription from the T7 promoter contained  
20 within the plasmids will give viral sense-strand transcripts.

Transcription reagents were obtained from Promega Corporation and protocols were performed as recommended by the manufacturer. To produce pIP-1 and pIP-2 RNAs  
25 encoding the HSV-1 and HSV-2 UL13 reading frames, respectively, plasmids pIP-1 and pIP-2 were linearized by digestion with restriction enzyme XbaI, which cuts the DNAs at a unique site 3' of the HSV DNA sequences which were cloned into pSP72. These linearized plasmids were  
30 used as template for *in vitro* transcription with T7 RNA polymerase. *In vitro* transcripts were purified by digestion of the template DNA with RQ1 DNase (20 minutes, 37°C), two extractions with phenol:chloroform: isoamyl alcohol (25:24:1), extraction with chloroform: isoamyl  
35 alcohol (24:1), precipitation in 3.75 M ammonium acetate

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and 70% ethanol, and resuspension in diethyl pyrocarbonate (DEPC)-treated water. The integrity and purity of the RNA preparations were verified by electrophoresis of an aliquot on a denaturing formaldehyde agarose gel according to standard procedures.

*In vitro* translation reagents were purchased from Promega Corporation. Translation reactions contained 120 ng of an appropriate RNA sample, 4  $\mu$ l of rabbit reticulocyte lysate, 1  $\mu$ l of a methionine-free amino acid mixture, 1  $\mu$ l of [<sup>35</sup>S] methionine (5  $\mu$ Ci, >1000 Ci/mmol, New England Nuclear), in a total volume of 12  $\mu$ l. The translation mixture was incubated for 1 hour at 37°C. After translation, 12  $\mu$ l of the translation mixture was added to 12  $\mu$ l of 2x Laemmli Loading Buffer (1x = 88 Tris-HCl, pH 6.8; 2% sodium dodecyl sulphate [SDS]; 5.0%  $\beta$ -mercaptoethanol; 10% glycerol; and 0.001% bromphenol blue), heated in a boiling water bath for 10 minutes, and the *in vitro* translation products were resolved by electrophoresis in a 10% polyacrylamide-SDS (Laemmli) gel. The resultant gels were dried under vacuum and autoradiography was performed using Kodak XRP-5 film. The RNA samples used for *in vitro* translation were preincubated for 1 hour at 37°C, with or without added oligonucleotide, immediately prior to addition into the translation mixture.

Oligonucleotides were synthesized on an automated DNA synthesizer (Applied Biosystems model 380B) using standard phosphoramidite chemistry as described in Example 1. For the phosphorothioate oligonucleotides, sulfurization was performed after each coupling using 0.2 M <sup>3</sup>H-1,2-Benzodithiol-3-one-1,1-dioxide dissolved in acetonitrile as described by Beaucage et al., *Ann. N.Y. Acad. Sc.* (1989). To insure complete thioation, the growing oligonucleotide was capped after each

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sulfurization step. For the methylphosphonate oligonucleotides, methyl phosphoramidite bases were obtained from Glen Research Corporation. All oligonucleotides were purified by lyophilization and two  
5 ethanol precipitations prior to use. The purity and integrity of the oligonucleotide preparation was determined by acrylamide gel electrophoresis.

For each experimental point in the clonogenic assay, HeLa cells (2500 cells in 5 ml of DMEM-10% FCS)  
10 were seeded in triplicate into 60 mm<sup>2</sup> tissue culture plates and incubated 18 hours at 37°C. After the overnight incubation, cells were overlaid with 1.5 ml of fresh medium, containing either ISIS 1082 or Acyclovir where appropriate, and incubated 3 days at 37°C. After  
15 the drug treatment, cells were overlaid with fresh medium and incubated for 6 days at 37°C prior to fixation and staining with crystal violet. To determine the toxic effect of compound upon the HeLa cells, stained cells were counted and compared to cell counts from parallel  
20 cultures of untreated HeLa cells.

The antiviral activity of various oligonucleotides containing different nucleotide sequences and backbone compositions were compared to the inhibitory activity of ISIS 1043 which has been shown to  
25 have anti-HSV activity in vitro . The oligodeoxyribonucleotide sequences, their target mRNA regions and the backbone composition of the oligonucleotides tested are listed in Table 8.

TABLE 8

Oligo Number	Backbone	Sequence	(SEQ ID NO.:)	Target	Gene	Location
5	P=O	GTCCGCGTCCATGTCGGC	1	HSV-1	UL48	AUG <sup>a</sup>
1043	P=O	GGACTCATCCATCCTTCGGCC	2	HSV-1	UL13	AUG-1 <sup>b</sup>
1044	P=O	GCGGCTGGCCATTCAACAGA	3	HSV-1	UL39	AUG
1045	P=O	CGCGGAATCCATGGCAGCAGG	4	HSV-1	UL40	AUG
1046	P=O	ACCGAGGTCCATGTCGTACGC	5	HSV-1	UL13	AUG-2
1047	P=O	GGACTCATCCATCCGTCGGCC	6	HSV-2	UL13	AUG-1
1048	P=O	GCGGAGGTCCATGTCGTACGC	7	HSV-2	UL13	AUG-2
10	P=S	GGACTCATCCATCCTTCGGCC	2	HSV-1	UL13	AUG-1 <sup>b</sup>
1049	P=S	GCGGCTGGCCATTCAACAGA	3	HSV-1	UL39	AUG
1076	P=S	CGCGGAATCCATGGCAGCAGG	4	HSV-1	UL40	AUG
1077	P=S	ACCGAGGTCCATGTCGTACGC	5	HSV-1	UL13	AUG-2
1078	P=S	GGACTCATCCATCCGTCGGCC	6	HSV-2	UL13	AUG-1
15	P=S	GCGGAGGTCCATGTCGTACGC	7	HSV-2	UL13	AUG-2
1080	P=S	GGACTCATCCATCCGTCGGCC	6	HSV-2	UL13	AUG-1
1081	P=S	GCGGAGGTCCATGTCGTACGC	7	HSV-2	UL13	AUG-2
1082	P=S	GGACTCATCCATCCGTCGGCC	6	HSV-2	UL13	AUG-1

<sup>a</sup> Draper et al., Antiviral Res. 13:151-164 (1990)

<sup>b</sup> UL13 AUG-1 is the primary translation initiation codon in the UL13 mRNA. UL13 AUG-2 is a second translation initiation codon which directs a low level of translational activity from the UL13 mRNA in in vitro translations.

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A viral multiplicity of 0.5 pfu/cell was used for these activity screens. A representative comparison of antiviral activities versus HSV-1 and HSV-2 is shown in Figure 10. Comparison of the antiviral effects of oligonucleotides with P=O backbones showed that the reduction of HSV infectious yield depended upon both the subtype of HSV used and the sequence of the oligonucleotide. The broadest antiviral activity was observed using ISIS 1049. Surprisingly, ISIS 1047, whose nucleotide sequence differs from ISIS 1049 only at the 5' terminal base, was not as effective as ISIS 1049 in inhibiting infectious virus yields. Although the trends of inhibition observed with the P=O oligonucleotides were consistent in all experiments, the absolute levels of inhibitory activity varied considerably (i.e., ISIS 1049 was invariably the best inhibitor of HSV replication, but the levels of inhibition ranged from a low of 18% to a high of 63% in 5 experiments). It was found that this variability was primarily due to differences in the temperature at which the fetal calf serum (FCS) was heat inactivated. The levels of inhibition shown in Figure 1 were obtained using FCS which had been heat-treated at 65°C. This treatment of the serum was standardized for all subsequent experiments.

Conversion of the oligonucleotide backbone from the P=O structure to the P=S structure resulted in greatly enhanced anti-HSV activity of all novel oligonucleotides tested (Figure 10). In contrast to the serum effects observed with P=O oligonucleotides and consistent with the increased resistance of P=S oligonucleotides to digestion by serum nucleases, it was found that the inhibitory activity of P=S oligonucleotides was independent of changes in the temperature of FCS heat-treatment.

Effect of Viral Multiplicity Upon  
ISIS 1082 Inhibition of HSV-1 Replication.

The effect of initial viral burden upon the antiviral activity of ISIS 1082 was examined using an infectious yield assay. Cells were infected at an MOI of either 0.05, 0.1, 0.25, 0.5, 1.0 or 2.5 pfu/cell, in the presence and absence of 4  $\mu$ M concentrations of ISIS 1082. ISIS 1082 was chosen for this experiment because of the broad anti-HSV activity of its analog, ISIS 1049, and the increased nuclease-resistance associated with P=S oligonucleotides. Infection of HeLa cells with HSV-1 across this range of multiplicities resulted in only a threefold increase of infectious virus production between the lowest MOI (0.05 pfu/cell) and the highest MOI (2.5 pfu/cell), while the range of multiplicities increased by 50-fold (Table 9).

TABLE 9

Input MOI <sup>a</sup> (pfu/cell)	ISIS 1082	Virus Yield (pfu/ml)	% Control Yield
2.5	-	$58.5 \pm 5.5 \times 10^7$	
	+	$56.5 \pm 6.0 \times 10^6$	9.7
1.0	-	$46.0 \pm 4.0 \times 10^7$	
	+	$44.5 \pm 0.5 \times 10^6$	9.7
0.5	-	$42.0 \pm 7.0 \times 10^7$	
	+	$71.0 \pm 3.0 \times 10^5$	1.7
0.25	-	$35.0 \pm 3.0 \times 10^7$	
	+	$11.1 \pm 0.5 \times 10^6$	3.2
0.1	-	$35.0 \pm 1.0 \times 10^7$	
	+	$18.5 \pm 3.5 \times 10^5$	0.5
0.05	-	$19.5 \pm 0.5 \times 10^7$	
	+	$15.5 \pm 3.5 \times 10^5$	0.8

<sup>a</sup> HSV-1 (strain KOS) was used for these experiments.

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Over this same range of multiplicities, the antiviral effect of ISIS 1082 varied from a low inhibition of 90.3% at a MOI of 1.0 pfu/cell, to the highest level of inhibition (99.5 %) at a MOI of 0.1 pfu/cell. Thus, when  
5 using MOIs between 0.1 and 1.0 pfu/cell, the amount of infectious virus produced did not reflect a simple mathematical relationship to the amount of input virus. However, the antiviral effect of ISIS 1082 was related inversely to the amount of input virus across this range of  
10 MOIs.

Effect of Backbone Composition Upon  
Antiviral Activity of Oligonucleotides

The effect of backbone composition upon the antiviral activity of oligonucleotides was examined by  
15 comparing different analogs of three oligonucleotide sequences in parallel assays. The nucleotide sequence of ISIS 1047 and a shortened version of this sequence, found in ISIS 1301, were synthesized with P=O, P=S and MeP backbones. The antiviral activities of these  
20 oligonucleotides in an infectious yield assay were compared to those of the MeP oligonucleotide described by Kulka et al., 1989. Proc. Natl. Acad. Sci. USA 86:6868-6872 and its P=S analog (Table 10).



TABLE 10

(SEQ ID NO.:	Sequence	Oligo	Backbone Linkage	% Control HSV-1 <sup>a</sup>	Yield HSV-2 <sup>b</sup>
5	ACCGAGGTCCATGTCGTACGC	1047 1237 1080	P=O MeP P=S	105 <sup>c</sup> 29.8 0.4	107 34.1 2.5
9	GAGGTCCATGTCGTA	1301 1277 1302	P=O MeP P=S	63.1 50.8 1.4	95.5 34.1 10.9
10	TTCTCTCCTGCGG <sup>d</sup>	1236 1235	MeP P=S	35.1 108	40.9 105

<sup>a</sup> HSV-1 (strain KOS) used at input MOI = 0.5 pfu/cell.

<sup>b</sup> HSV-2 (strain HG52) used at input MOI = 0.5 pfu/cell.

<sup>c</sup> All oligonucleotides were applied at a concentration of 4  $\mu$ M. The values used to determine percent control yield were achieved by calculating the average of duplicate titrations from a pooled sample of 2-3 experiments. All oligonucleotides gave >99% inhibition at concentrations of 100  $\mu$ M.

<sup>d</sup> The methylphosphonate analog of this oligonucleotide sequence was previously reported to exhibit anti-HSV activity in a plaque reduction assay.

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At oligonucleotide concentrations of either 4  $\mu$ M or 100  $\mu$ M, the degree of inhibition of HSV-1 progenesis was roughly equivalent for each of the methylphosphonate oligonucleotides (ISIS 1237, 1277 and 1236). At an  
5 oligonucleotide concentration of 4  $\mu$ M, the anti-HSV activities shown by the MeP oligonucleotides were similar with both subtypes of HSV tested. For ISIS 1237 and 1277, the antiviral activities of the MeP analogs were better than those observed with the corresponding P=O analogs,  
10 ISIS 1047 and 1301, respectively. Phosphorothioate analogs of the 21- and 15-nucleotide sequences (ISIS 1080 and ISIS 1302, respectively), exhibited greatly enhanced antiviral activity over that observed when using either ISIS 1237 or ISIS 1277. Surprisingly, neither HSV-1 nor HSV-2  
15 replication was inhibited by ISIS 1235, the P=S analog of ISIS 1236. Comparatively, the level of antiviral activity was affected more profoundly by changes in composition of the oligonucleotide backbone or nucleotide sequence than by differences in the length of the oligonucleotide.

20 Effect of ISIS 1049 and 1082 Upon  
In Vitro Translation of UL13RNA

The ability of ISIS 1049 and 1082 oligonucleotides to bind specifically to target UL13 RNA (pIP-1 or pIP-2 transcript) and inhibit translation was  
25 examined using rabbit reticulocyte lysates for in vitro translations. ISIS 1238, which consists of a scrambled version of the ISIS 1080 nucleotide sequence, was included as a control for nonspecific phosphorothioate oligonucleotide effects upon translational activity. An in  
30 vitro synthesized transcript (5LO) containing the RNA sequence of the human 5-lipoxygenase transcript was used to determine the effect of the ISIS oligonucleotides upon translation of heterologous RNAs.

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Translation of pIP-1 RNA (Figure 11A) resulted in the synthesis of a major polypeptide product of approximately 61 kD mass and a number of lesser products, most notably a polypeptide of 33 kD mass which is initiated from the secondary AUG codon region complementary to the ISIS 1080 (1082) and 1047 (1049) oligonucleotides. Quantitatively, ISIS 1049 was a better inhibitor of the translation of pIP-1 RNA than ISIS 1082, which in turn was a better inhibitor than ISIS 1238. Qualitatively, the inhibition of pIP-1 RNA translation by ISIS 1049 and 1082 appears to be operating by slightly different molecular mechanisms. With both ISIS 1082 and 1049, the addition of oligonucleotide results in a reduction of the quantity of full length polypeptide synthesized from pIP-1 RNA. Additionally, inhibition with ISIS 1049 results in observable increases of three smaller polypeptide products of 33, 28, and 26 kD mass. The 33 kD polypeptide is the same polypeptide which is synthesized at low levels in the nontreated samples. The 28 kD polypeptide is believed to be a truncated version of the 61 kD and the 26 kD polypeptide is believed to be initiated at another in-phase AUG which is located 3' to the ISIS 1049 target region. Similar patterns of inhibition were observed when both the homologous *in vitro* transcript from pIP-2 (Figure 11B) was substituted for pIP-1 RNA in the hybridization mixture and when translations were performed using wheat germ lysates.

Nonspecific inhibitory effects of oligonucleotides upon the translation of RNA were minimal. ISIS 1238 exhibited a slight, but detectable inhibition of the translation of pIP-1 RNA, while none of the oligonucleotides were inhibitory to the translation of the heterologous 5LO RNA.

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Comparative Antiviral Effects of Acyclovir and  
ISIS Oligonucleotides Upon HSV-2 Replication

Dose response curves for Acyclovir (ACV), ISIS 1302, ISIS 1080, and ISIS 1082 versus HSV-2 (strain HG52) were determined using the infectious yield assay. Because the ACV stock solutions (4 mM) were dissolved in dimethyl sulfoxide (DMSO), virus titers of the ACV-treated samples were compared to titers from control infections which were treated with 0.025% DMSO. The control virus yield calculated for DMSO-treated samples was approximately 30% greater than the yield observed in untreated samples. Representative dose response curves are shown in Figure 13. Each of the four compounds affected HSV-2 replication in a dose-dependent manner. From the data shown in Figure 12, the  $IC_{50}$  values for these compounds were calculated to be 600 mM, 2  $\mu$ M, 430 nM and 250 nM, respectively, for ACV, ISIS 1302, ISIS 1082 and ISIS 1080. The slopes of the dose response curves for ISIS 1080 and 1082 changed when other strains of HSV-1 or HSV-2 were used in the infection (e.g., see Figure 12).

Dose Dependent Effect of ISIS 1082 Upon  
Replication of Two Strains of HSV-1

The antiviral efficacy of ISIS 1082 versus two strains of HSV-1, KOS and F, was compared to the antiviral efficacy of both a known anti-HSV compound, ACV, and a noncomplementary phosphorothioate oligonucleotide, ISIS 1238; this oligonucleotide comprises a scrambled version of ISIS 1080, serving as a control for nonspecific oligonucleotide effects on translational activity. ISIS 1238 was much less inhibitory than either ISIS 1082 or ACV in these studies. ISIS 1082 and ACV inhibited the KOS strain with predicted  $IC_{90}$ s of 2.73 and 2.57  $\mu$ M, respectively (Figure 13). The  $IC_{90}$ s of ACV and ISIS 1082 were extrapolated to be 3.6 and 5.8  $\mu$ M, respectively for the F strain of the virus (Figure 14). Although the  $IC_{90}$

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values of ACV and ISIS 1082 are similar for both virus strains, the dose response curves show that strain-specific patterns of inhibition exist among HSV strains treated with these compounds.

5 Dose Dependent Effect of ISIS 1082 Upon  
Replication of ACV-Resistant Strains of HSV-1

The antiviral efficacy of ISIS 1082 was examined using two ACV<sup>r</sup> strains of HSV-1, the DM2.1 strain which is devoid of the viral thymidine kinase gene and the PAAr<sup>5</sup> strain which expresses an altered nucleotide binding site in the viral DNA polymerase. Both virus strains were treated with ISIS 1082 at concentrations of 400 nM, 800 nM or 4  $\mu$ M. For comparison, each strain was treated in parallel infections with the same concentrations of ACV. At the concentrations tested, ACV affected neither strain in a dose-dependent manner while treatment with ISIS 1082 inhibited viral yield of both strains in a dose-dependent manner (Figure 15). The IC<sub>50</sub> values for ISIS 1082 were predicted from this data to be 300 nM and 600 nM with the DM2.1 and PAAr<sup>5</sup> strains of HSV-1, respectively. The reduction in yield of the DM2.1 strain at levels similar to those observed when treating other strains of HSV-1 (Figure 13, 14) or HSV-2 (Figure 12) demonstrated that the antiviral effect of ISIS 1082 does not require phosphorylation of the oligonucleotide by the viral thymidine kinase enzyme.

Comparative Cellular Toxicities of ISIS 1082 and ACV

The cellular toxicities of ISIS 1082 and ACV were evaluated using a clonogenic assay in HeLa cells which reflected the time of compound exposure used for the infectious yield assays. At compound concentrations 100  $\mu$ M, neither ISIS 1082 nor ACV caused a 50% reduction in the clonogenic capacity of HeLa cells in the assays. Using the average IC<sub>50</sub> values of 275 nM and 300 nM for ISIS 1082 and

- 55 -

ACV, respectively, versus HSV-2 (Figure 12), the  
Therapeutic Indices (TIs,  $TI = LC_{50}/IC_{50}$ ) of the compounds  
were calculated to be >360 for ISIS 1082 and >334 for ACV.  
Thus, the predicted TI for ISIS 1082 from these studies was  
5 comparable to that of ACV.

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## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Draper et al.
- (ii) TITLE OF INVENTION: Oligonucleotide Therapies for  
Modulating the Effects of Herpesviruses
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Woodcock Washburn Kurtz  
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  - (B) STREET: One Liberty Place - 46th Floor
  - (C) CITY: Philadelphia
  - (D) STATE: PA
  - (E) COUNTRY: USA
  - (F) ZIP: 19103
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
  - (B) COMPUTER: IBM PS/2
  - (C) OPERATING SYSTEM: PC-DOS
  - (D) SOFTWARE: WORDPERFECT 5.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: n/a
  - (B) FILING DATE: herewith
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 485,297

- 57 -

(B) FILING DATE: February 26, 1990

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Jane Massey Licata

(B) REGISTRATION NUMBER: 32,257

(C) REFERENCE/DOCKET NUMBER: ISIS-0085

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (215) 568-3100

(B) TELEFAX: (215) 568-3439

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(iv) ANTI-SENSE: Y

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GTCCGCGTCC ATGTCGGC 18

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(iv) ANTI-SENSE: Y

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GGACTCATCC ATCCTTCGGC C 21



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## (2) INFORMATION FOR SEQ ID NO: 3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(iv) ANTI-SENSE: Y

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCGGCTGGCC ATTCAACAG A 21

## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(iv) ANTI-SENSE: Y

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CGCGGAATCC ATGGCAGCAG G 21

## (2) INFORMATION FOR SEQ ID NO: 5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(iv) ANTI-SENSE: Y

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ACCGAGGTCC ATGTCGTACG C 21

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## (2) INFORMATION FOR SEQ ID NO: 6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(iv) ANTI-SENSE: Y

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GGACTCATCC ATCCGTCCGC C 21

## (2) INFORMATION FOR SEQ ID NO: 7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(iv) ANTI-SENSE: Y

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GCCGAGGTCC ATGTCGTACG C 21

## (2) INFORMATION FOR SEQ ID NO: 8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(iv) ANTI-SENSE: Y

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GCGGTTGGCC ATTGGAACCA A 21

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## (2) INFORMATION FOR SEQ ID NO: 9:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GAGGTCCATG TCGTA 15

## (2) INFORMATION FOR SEQ ID NO: 10:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

TTCCTCCTGC GG 12

## (2) INFORMATION FOR SEQ ID NO: 11:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1557

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATGGATGAGT CCCGACAGACA GCGACCTGCT GGTCATGTGG CAGCTA

CAGCCCCCAA GGTGCACGCC AACGGTCCTT CAAGGATTGG CTCGCA

ACGTACACTC CAACCCCCAC GGGGCCTCCG GGCGCCCCAG CGGCCCC

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CTCCAGGACG CCGCCGTCTC CCGCTCCTCC CACGGGTCCC GCCACCGATC 200  
CGGCCTCCGC GAGCGGCTTC GCGCGGGACT ATCCCGATGG CGAATGAGCC 250  
GCTCGTCTCA TCGCCGCGCG TCCCCCGAGA CGCCCGGTAC GGCGGCCAAA 300  
CTGAACCGCC CGCCCCTGCG CAGATCCCAG GCGGCGTTAA CCGCACCCCC 350  
CTCGTCCCCC TCGCACATCC TCACCCTCAC GCGCATCCGC AAGCTATGCA 400  
GCCCCGTGTT CGCCATCAAC CCCGCCCTAC ACTACACGAC CCTCGAGATC 450  
CCCGGGGCCC GAAGCTTCGG GGGGTCTGGG GGATACGGTG ACGTCCAACT 500  
GATTCGCGAA CATAAGCTTG CCGTTAAGAC CATAAAGGAA AAGGAGTGGT 550  
TTGCCGTTGA GCTCATCGCG ACCCTGTTGG TCGGGGAGTG CGTTCTACGC 600  
GCCGGCCGCA CCCACAACAT CCGCGGCTTC ATCGCGCCCC TCGGGTTCTC 650  
GCTGCAACAA CGACAGATAG TGTTCGCCGC GTACGACATG GACCTCGGTA 700  
AGTATATCGG CCAACTGGCG TCCCTGCGCA CAACAAACCC CTCGGTCTCG 750  
ACGGCCCTCC ACCAGTGCTT CACGGAGCTG GCCCGCGCCG TTGTGTTTTT 800  
AAACACCACC TCGGGGATCA GCCACCTGGA TATCAAGTGC GCCAACATCC 850  
TCGTCATGCT GCGGTCGGAC GCCGTCTCGC TCCGGCGGGC CGTCCTCGCC 900  
GACTTTAGCC TCGTCACCCT CAACTCCAAC TCCACGATCG CCCGGGGGCA 950  
GTTTTGCCTC CAGGAGCCGG ACCTCAAGTC CCCCCGGATG TTTGGCATGC 1000  
CCACCGCCCT AACCACAGCC AACTTTCACA CCCTGGTGGG TCACGGGTAT 1050  
AACCAGCCCC CGGAGCTGTT GGTGAAATAC CTTAACAACG AACGGGCCGA 1100  
ATTTACCAAC CACCGCCTGA AGCACGACGT CGGGTTAGCG GTTGACCTGT 1150  
ACGCCCTGGG CCAGACGCTG CTGGAGTTGG TGGTTAGCGT GTACGTCGCC 1200  
CCGAGCCTGG GCGTACCCGT GACCCGGTTT CCCGGTTACC AGTATTTTAA 1250  
CAACCAGCTG TCGCCGGA CTGCCCTGGC CCTGCTCGCC TATCGCTGCG 1300  
TGCTGCACCC AGCCCTGTTT GTCAACTCGG CCGAGACCAA CACCACGGC 1350  
CTGGCGTATG ACGTCCCAGA GGGCATCCGG CGCCACCTCC GCAATCCCAA 1400  
GATTCGGCGC GCGTTTACGG ATCGGTGTAT AAATTACCAG CACACACACA 1450  
AGGCGATACT GTCGTCGGTG GCGCTGCCTC CCGAGCTTAA GCCTCTCCTG 1500

- 62 -

GTGCTGGTGT CCCGCCTGTG TCACACCAAC CCGTGCGCGC GGCACGCGCT 1550  
GTCGTGA 1557

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1557
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

ATGGATGAGT CCGGGCGACA GCGACCTGCT GGTCGTGTGG CAGCTGACAT 50  
CAGCCCCCAA GGTGCACACC GACGCTCCTT CAAGGCCTGG CTCGCGTCCT 100  
ACATACTCTC CCTCAGCCGC CGGGCGTCCG GACGCCCAAG CGGCCCCTCC 150  
CCCCGAGACG GCGCCGTCTC CGGAGCCCGC CCCGGGTCCC GCCGCCGATC 200  
CAGCTTCCGG GAGCGGCTTC GCGCGGGACT GTCCCGATGG CGAGTGAGCC 250  
GCTCGTCTCG TCGCCGCTCG TCCCCGAGG CCCCCGGCCC TCGGGCCAAG 300  
CTAAGGCGCC CGCCCCTGCG CAGGTCCGAG ACGGCCATGA CCTCGCCCCC 350  
GTCGCCCCCC TCGCACATCC TGTCCCTCGC GCGCATCCAC AAGCTATGCA 400  
TCCCCGTATT CGCCGTCAAC CCCGCCCTCC GCTACACGAC CTCGGAGATC 450  
CCCGGGGCCC GCAGCTTCGG GGGCTCGGGG GGGTACGGCG AGGTGCAGTT 500  
GATTCGCGAA CACAACTCG CCGTGAAGAC CATCCGGGAA AAAGAGTGGT 550  
TTGCCGTGGA GCTCGTCGCG ACCCTGCTCG TGGGGGAGTG CGCTCTTCGC 600  
GGCGGCCGCA CCCACGACAT CCGCGGCTTT ATCACCCCGC TCGGGTTCTC 650  
GCTGCAGCAG CGCCAGATCG TGTTCCTCCG GTACGACATG GACCTCGGCA 700  
AGTACATCGG CCAGCTGGCG TCCCTGCGCG CGACCACCCC CTCCGTTCGG 750  
ACGGCCCCTCC ACCACTGCTT CACAGACCTG GCGCGCGCCG TGGTGTTCCT 800  
GAACACCAGG TCGGGGATCA GCCACCTGGA CATCAAGTGC GCCAACGTCC 850  
TCGTGATGCT GCGATCGGAC GCGGTGTCGC TCCGGCGGGC CGTCCTGGCC 900

- 63 -

GACTTTAGCC TGGTGACCCT GAACTCCAAC TCCACGATAT CCCGGGGCCA 950  
GTTTTGCCTC CAGGAGCCGG ACCTCGAGTC CCCCCGGGGG TTTGGGATGC 1000  
CCGCCGCCCT GACCACGGCC AACTTTCACA CTCTGGTGGG GCACGGGTAC 1050  
AACCAGCCAC CGGAGCTCTC GGTAAGTAC CTCAACAACG AGCGGGCCGA 1100  
GTTTAACAAC CGCCCCCTGA AGCACGACGT CGGGCTGGCG GTCGATCTCT 1150  
ACGCCCTGGG GCAGACGCTG CTGGAGCTGC TGGTTAGCGT GTACGTGGCC 1200  
CCGAGCCTGG GCGTCCCCGT GACCCGCGTC CCGGGCTACC AGTACTTTAA 1250  
CAACCAGCTC TCGCCGACT TTGCCGTGGC CCTCCTCGCC TATCGCCGCG 1300  
TTCTGCACCC CGCCCTCTTT GTCAACTCGG CCGAGACCAA CACCCACGGC 1350  
CTGGCGTATG ACGTGCCGGA GGGCATCCGG CGCCACCTTC GCAATCCCAA 1400  
GATTCGGCGC GCGTTCACGG AGCAGTGTAT AAATTACCAG CGCACGCACA 1450  
AGGCCGTCCT GTCGTCGGTG TCGCTGCCGC CCGAGCTGAG GCCGCTGCTG 1500  
GTGCTGGTCT CCCGCCTCTG TCACGCCAAC CCGGCCGCGC GCCACTCTCT 1550  
GTCGTGA 1557

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**WHAT IS CLAIMED IS:**

1. An oligonucleotide or oligonucleotide analog specifically hybridizable with RNA or DNA deriving from a gene corresponding to one of the open reading frames UL5,  
5 UL8, UL9, UL13, UL29, UL30, UL39, UL40, UL42 AND UL52 of herpes simplex virus type 1, said oligonucleotide comprising nucleotide units sufficient in identity and number to effect said specific hybridization.
2. The oligonucleotide of claim 1 specifically  
10 hybridizable with a translation initiation site.
3. The oligonucleotide of claim 1 comprising a sequence CAT.
4. The oligonucleotide of claim 1 wherein the gene is from herpes simplex virus type 1, herpes simplex virus type  
15 2, cytomegalovirus, human herpes virus 6, Epstein Barr virus or varicella zoster virus.
5. The oligonucleotide of claim 1 in a pharmaceutically acceptable carrier.
6. The oligonucleotide of claim 1 wherein at least some  
20 of the linking groups between nucleotide units of the oligonucleotide comprise sulfur-containing species.
7. The oligonucleotide of claim 1 wherein at least some of the linking groups between nucleotide units of the oligonucleotide comprise phosphorothioate moieties.

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25 8. An oligonucleotide comprising one of the sequences:

5'-

-3'

GGA CTC ATC CAT CCT TCG GCC, SEQ ID NO.: 2,

GCG GCT GGC CAT TTC AAC AGA, SEQ ID NO.: 3,

CGC GGA ATC CAT GGC AGC AGG, SEQ ID NO.: 4,

30 ACC GAG GTC CAT GTC GTA CGC, SEQ ID NO.: 5,

GGA CTC ATC CAT CCG TCC GCC, SEQ ID NO.: 6,

GCC GAG GTC CAT GTC GTA CGC, SEQ ID NO.: 7, and

GCG GTT GGC CAT TGG AAC CAA, SEQ ID NO.: 8.

9. The oligonucleotide of claim 8 in a pharmaceutically  
35 acceptable carrier.

10. The oligonucleotide of claim 8 wherein at least some  
of the linking groups between nucleotide units of the  
oligonucleotide comprise sulfur-containing species.

11. The oligonucleotide of claim 8 wherein at least some  
40 of the linking groups between nucleotide units of the  
oligonucleotide comprise phosphorothioate moieties.

12. A method of modulating the activity of a herpesvirus  
comprising contacting the virus or an animal infected with  
the virus with an oligonucleotide specifically hybridizable  
45 with RNA or DNA deriving from a gene corresponding to one  
of the open reading frames UL5, UL8, UL9, UL13, UL29, UL30,  
UL39, UL40, UL42 AND UL52 of herpes simplex virus type 1,  
said oligonucleotide comprising nucleotide units sufficient  
in identity and number to effect said specific  
50 hybridization.

13. The method of claim 12 wherein the oligonucleotide  
is specifically hybridizable with a translation initiation  
site.



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14. The method of claim 12 wherein the oligonucleotide  
55 comprises the sequence CAT.

15. The method of claim 12 wherein the herpesvirus is  
herpes simplex virus type 1, herpes simplex virus type 2,  
cytomegalovirus, human herpes virus 6, Epstein Barr virus  
or varicella zoster virus.

60 16. The method of claim 12 wherein the oligonucleotide  
comprises one of the sequences:

5'-

-3'

GGA CTC ATC CAT CCT TCG GCC, SEQ ID NO.: 2,  
GCG GCT GGC CAT TTC AAC AGA, SEQ ID NO.: 3,  
65 CGC GGA ATC CAT GGC AGC AGG, SEQ ID NO.: 4,  
ACC GAG GTC CAT GTC GTA CGC, SEQ ID NO.: 5,  
GGA CTC ATC CAT CCG TCC GCC, SEQ ID NO.: 6,  
GCC GAG GTC CAT GTC GTA CGC, SEQ ID NO.: 7, and  
GCG GTT GGC CAT TGG AAC CAA, SEQ ID NO.: 8.

70 17. The method of claim 12 wherein at least some of the  
linking groups between nucleotide units of the  
oligonucleotide comprise sulfur-containing species.

18. The method of claim 12 wherein at least some of the  
linking groups between nucleotide units of the  
75 oligonucleotide comprise phosphorothioate moieties.

19. A method of treating an animal suspected of having a  
herpesvirus infection comprising contacting the animal with  
an oligonucleotide specifically hybridizable with RNA or  
DNA deriving from a gene corresponding to one of the open  
80 reading frames UL5, UL8, UL9, UL13, UL29, UL30, UL39, UL40,  
UL42 AND UL52 of herpes simplex virus type 1, said  
oligonucleotide comprising nucleotide units sufficient in  
identity and number to effect said specific hybridization.

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20. The method of claim 19 wherein said oligonucleotide  
85 is specifically hybridizable with a translation initiation  
site.

21. The method of claim 19 wherein said oligonucleotide  
comprises the sequence CAT.

22. The method of claim 19 wherein said herpesvirus is  
90 herpes simplex virus type 1, herpes simplex virus type 2,  
cytomegalovirus, human herpes virus 6, Epstein Barr virus  
or varicella zoster virus.

23. The method of claim 19 wherein the oligonucleotide  
is in a pharmaceutically acceptable carrier.

95 24. The method of claim 19 wherein the oligonucleotide  
comprises one of the sequences:

5'-

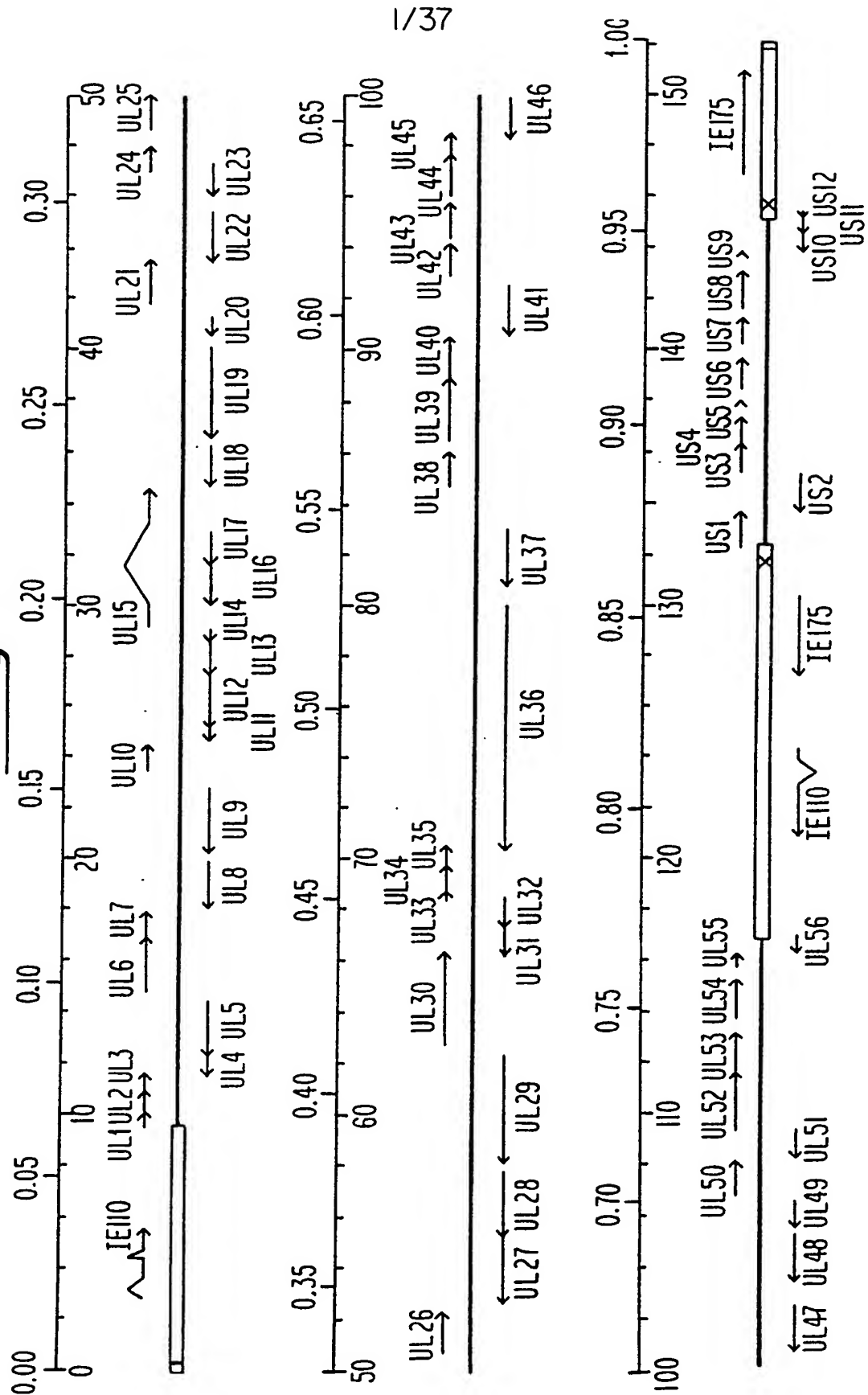
-3'

GGA CTC ATC CAT CCT TCG GCC, SEQ ID NO.: 2,  
GCG GCT GGC CAT TTC AAC AGA, SEQ ID NO.: 3,  
100 CGC GGA ATC CAT GGC AGC AGG, SEQ ID NO.: 4,  
ACC GAG GTC CAT GTC GTA CGC, SEQ ID NO.: 5,  
GGA CTC ATC CAT CCG TCC GCC, SEQ ID NO.: 6,  
GCC GAG GTC CAT GTC GTA CGC, SEQ ID NO.: 7, and  
GCG GTT GGC CAT TGG AAC CAA, SEQ ID NO.: 8.

105 25. The method of claim 19 wherein at least some of the  
linking groups between nucleotide units of the  
oligonucleotide comprise sulfur-containing species.

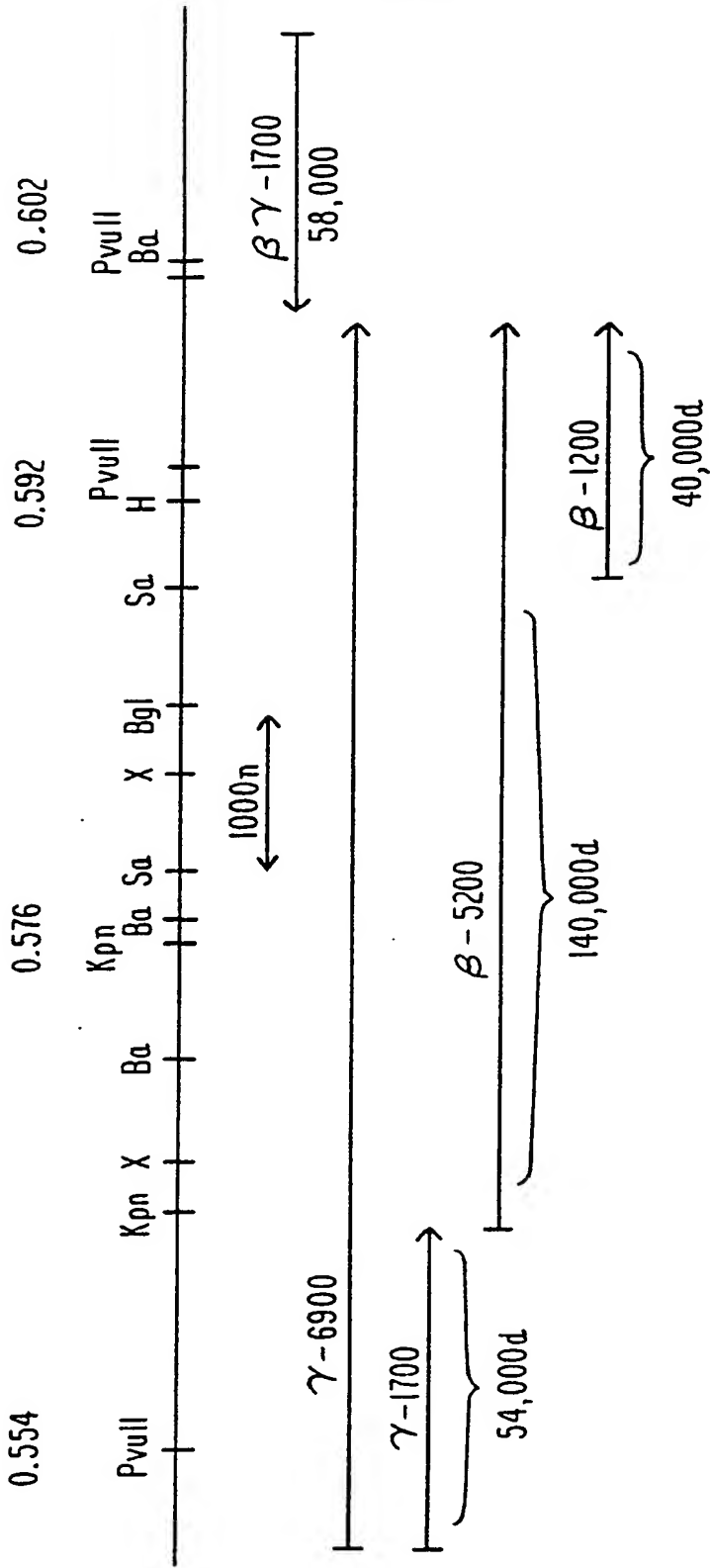
26. The method of claim 19 wherein at least some of the  
linking groups between nucleotide units of the  
110 oligonucleotide comprise phosphorothioate moieties.

**Fig. 1**

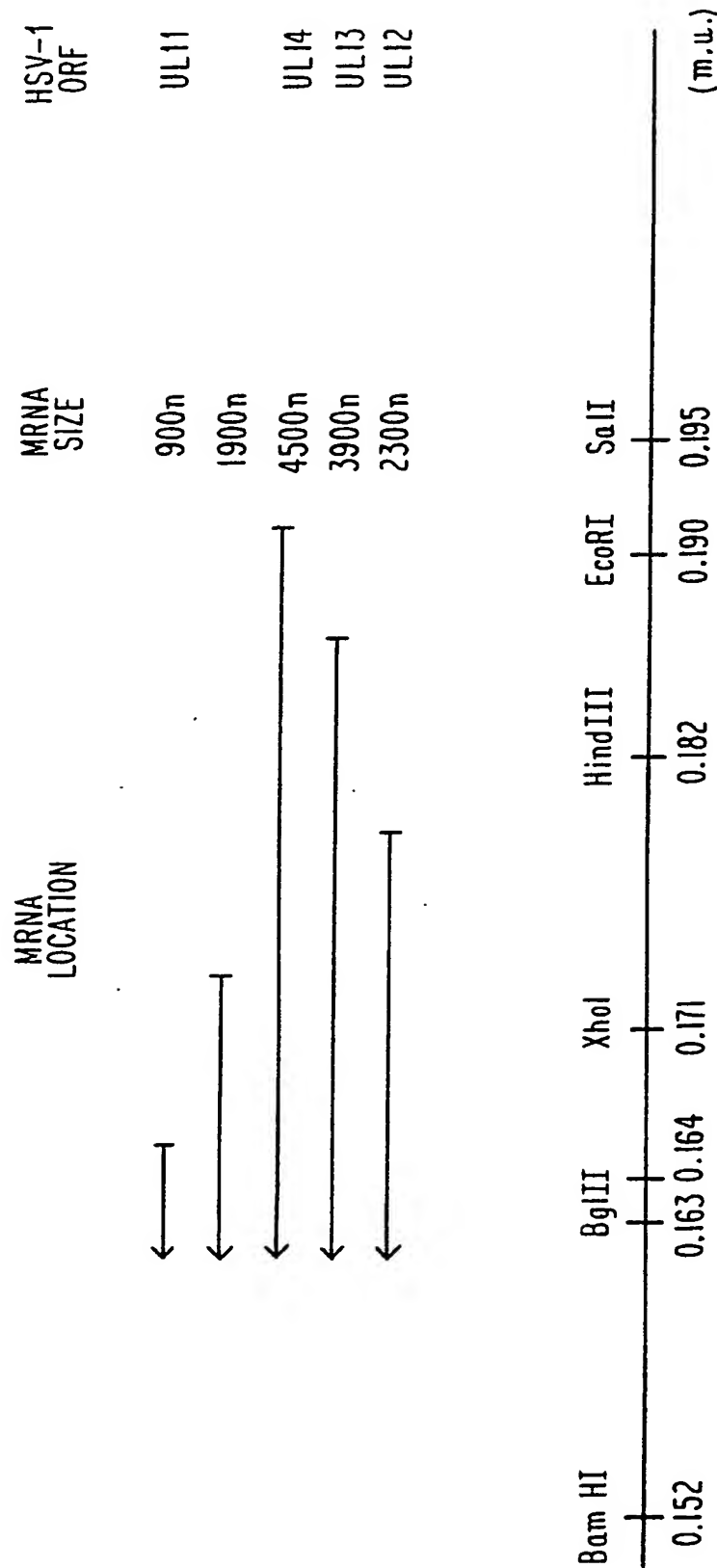


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***Fig. 2A***



***Fig. 2B***

base no.	1						50
HSV-1	ATGGATGAGT	CCGCAGACA	GGACCTGCT	GGTCATGTGG	CAGCTAACCT		
HSV-2	ATGGATGAGT	CCGGCGACA	GGACCTGCT	GGTCGTGTGG	CAGCTGACAT		
Matches	ATGGATGAGT	CC-G--GACA	GGACCTGCT	GGTC-TGTGG	CAGCT-AC-T		
	51					100	
HSV-1	CAGCCCCCAA	GGTGACGCC	AACGGTCCTT	CAAGGATTGG	CTCGCATCCT		
HSV-2	CAGCCCCCAA	GGTGACACC	GACGTCCTT	CAAGGCCCTGG	CTCGCGTCCT		
Matches	CAGCCCCCAA	GGTGAC-CC	-ACG-TCCTT	CAAGG--TGG	CTCGC-TCCT		
	101					150	
HSV-1	ACGTACACTC	CAACCCCCAC	GGGCGCTCCG	GGCGCCCCAG	CGGCCCTCT		
HSV-2	ACATACACTC	CCTCAGCCGC	CGGCGTCCG	GACGCCCAAG	CGGCCCTCTC		
Matches	AC-TACACTC	C--C--CC-C	-GGGC-TCCG	G-CGCC-AG	CGGCCCTC-4/37		
	151					200	
HSV-1	CTCCAGGACG	CCGCCGTCTC	CCGCTCCTCC	CACGGGTCCC	GCCACCGATC		
HSV-2	CCCCGAGACG	GGCCGTCTC	CGAGCCCGC	CCCGGTCCC	GCCGCCGATC		
Matches	C-CC--GACG	-CGCCGTCTC	C-G--CC--C	C-CGGGTCCC	GCC-CCGATC		
	201					250	
HSV-1	CGGCCTCCGC	GAGCGGCTTC	GCGCGGACT	ATCCCCGATGG	CGAATGAGCC		
HSV-2	CAGCTTCCGG	GAGCGGCTTC	GCGCGGACT	GTCCCCGATGG	CGAGTGAGCC		
Matches	C-GC-TCCG-	GAGCGGCTTC	GCGCGGACT	-TCCCCGATGG	CGA-TGAGCC		
	251					300	
HSV-1	GCTCGTCTCA	TCGCCGCGCG	TCCCCCGAGA	CGCCCCGTAC	GGCGGCCAAA		
HSV-2	GCTCGTCTCG	TCGCCGCTCG	TCCCCCGAGG	CCCCCGCCC	TGCGGCCAAG		
Matches	GCTCGTCTC-	TCGCCG-CG	TCCCCCGAG-	C-CCCCG--C	-GGCGGCCAA-		

***Fig. 3A***

HSV-1	301	CTGAACCGCC	CGCCCTCGG	CAGATCCCAG	GCGGCGTTAA	CCGCACCCCC	350
HSV-2		CTAAGCGGCC	CGCCCTCGG	CAGGTCCGAG	ACGGCCATGA	CCTCGCCCCC	
Matches		CT-A--CGCC	CGCCCTCGG	CAG-TCC-AG	-CGGC--T-A	CC-C-CCCC	
HSV-1	351	CTCGTCCCC	TCGCACATCC	TCACCCCTCAC	GCGCATCCGC	AAGCTATGCA	400
HSV-2		GTCGCCCCCC	TCGCACATCC	TGTCCCTCGC	GCGCATCCAC	AAGCTATGCA	
Matches		-TCG-CCCC	TCGCACATCC	T--CCCTC-C	GCGCATCC-C	AAGCTATGCA	
HSV-1	401	GCCCCGTGTT	CGCCATCAAC	CCCGCCCTAC	ACTACACGAC	CCTCGAGATC	450
HSV-2		TCCCCGTATT	CGCGTCAAC	CCCGCCCTCC	GCTACACGAC	CTCGGAGATC	
Matches		-CCCCGT-TT	CGCC-TCAAC	CCCGCCCT-C	-CTACACGAC	C---GAGATC <sup>37</sup>	
HSV-1	451	CCCGGGGCC	GAAGCTTCGG	GGGTCTGGG	GGATACGGTG	ACGTCCAACT	500
HSV-2		CCCGGGGCC	GCAGCTTCGG	GGGTCTGGG	GGTACGGCG	AGGTGCAGTT	
Matches		CCCGGGGCC	G-AGCTTCGG	GGG-TG-GGG	GG-TACGG-G	A-GT-CA--T	
HSV-1	501	GATTCGCGAA	CATAAGCTTG	CCGTAAAGAC	CATAAAGGAA	AAGGAGTGGT	550
HSV-2		GATTCGCGAA	CACAAACTCG	CCGTGAAGAC	CATCCGGGAA	AAAGAGTGGT	
Matches		GATTCGCGAA	CA-AA-CT-G	CCGT-AAGAC	CAT---GGAA	AA-GAGTGGT	
HSV-1	551	TTGCCCGTTGA	GCTCATCGCG	ACCTGTGTTG	TCGGGGAGTG	CGTTCACGC	600
HSV-2		TTGCCCGTGA	GCTCGTCGCG	ACCTGTCTCG	TGGGGAGTG	CGCTCTTCGC	
Matches		TTGCCCGT-GA	GCTC-TCGCG	ACCTG-T-G	T-GGGGAGTG	CG-TCT-CGC	

***Fig. 3B***

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HSV-1	601	GCCGGCCGCA	CCCACAACAT	CCGCGGCTTC	ATCGCGCCCC	TCGGGTCTCTC	650
HSV-2		GGCGGCCGCA	CCCACGACAT	CCGCGGCTTT	ATCACCCCGC	TCGGGTCTCTC	
Matches		G-CGGCCGCA	CCCAC-ACAT	CCGCGGCTT-	ATC-C-CC-C	TCGGGTCTCTC	
	651						700
HSV-1		GCTGCAACAA	CGACAGATAG	TGTTCCCCCG	GTACGACATG	GACCTCGGTA	
HSV-2		GCTGCAGCAG	CGCCAGATCG	TGTTCCCCCG	GTACGACATG	GACCTCGGCA	
Matches		GCTGCA-CA-	CG-CAGAT-G	TGTTCCCCCG	GTACGACATG	GACCTCGG-A	
	701						750
HSV-1		AGTATATCGG	CCAAGTGGCG	TCCCTGCGCA	CAACAAACCC	CTCGGTCTCG	
HSV-2		AGTACATCGG	CCAGCTGGCG	TCCCTGCGCG	CGACCAACCC	CTCCGTGCGG	
Matches		AGTA-ATCGG	CCA-CTGGCG	TCCCTGCGC-	C-AC-A-CCC	CTC-GTC-CG	
	751						800
HSV-1		ACGGCCCTCC	ACCAGTGCTT	CACGGAGCTG	GCCCGCGCCG	TTGTGTTT	
HSV-2		ACGGCCCTCC	ACCAGTGCTT	CACAGACCTG	GCGCGCGCCG	TGGTGTTCCT	
Matches		ACGGCCCTCC	ACCA-TGCTT	CAC-GA-CTG	GC-CGCGCCG	T-GTGT--T	
	801						850
HSV-1		AAACACCA	TGCGGGATCA	GCCACCTGGA	TATCAAGTGC	GCCAAACATCC	
HSV-2		GAACACCA	TGCGGGATCA	GCCACCTGGA	CATCAAGTGC	GCCAAACGTCC	
Matches		-AACACCA--	TGCGGGATCA	GCCACCTGGA	-ATCAAGTGC	GCCAAAC-TCC	
	851						900
HSV-1		TCGTTCATGCT	GCGTTCGGAC	GCCGTCTCGC	TCCGGCGGGC	CGTCCTCGCC	
HSV-2		TCGTGATGCT	GCGATCGGAC	GCGGTGTCGC	TCCGGCGGGC	CGTCCTGGCC	
Matches		TCGT-ATGCT	GCG-TCGGAC	GC-GT-TCGC	TCCGGCGGGC	CGTCCT-GCC	

***Fig. 3C*****SUBSTITUTE SHEET**



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HSV-1	901	GACTTTAGCC	TCGTCAACCCT	CAACTCCAAC	TCCACGATCG	CCCCGGGGCA	950
HSV-1		GACTTTAGCC	TGGTGACCCCT	GAACTCCAAC	TCCACGATAT	CCCCGGGGCCA	
Matches		GACTTTAGCC	T-GT-ACCCT	-AACTCCAAC	TCCACGAT--	CCCCGGG-CA	
HSV-1	951	GTTTGGCCTC	CAGGAGCCGG	ACCTCAAGTC	CCCCCGGATG	TTTGGCATGC	1000
HSV-2		GTTTGGCCTC	CAGGAGCCGG	ACCTCGAGTC	CCCCCGGGG	TTTGGGATGC	
Matches		GTTTGGCCTC	CAGGAGCCGG	ACCTC-AGTC	CCCCCGG--G	TTTGG-ATGC	
HSV-1	1001	CCACCGCCCT	AACCACAGCC	AACTTTCACA	CCCTGGTGGG	TCACGGGTAT	1050
HSV-2		CCGCCGCCCT	GACCACGGCC	AACTTTCACA	CTCTGGTGGG	GCACGGGTAC	
Matches		CC-CCGCCCT	-ACCAC-GCC	AACTTTCACA	C-CTGGTGGG	-CACGGGTA-	
HSV-1	1051	AACCAGCCCC	CGGAGCTGTT	GGTGAAATAC	CTTAACAACG	AACGGGCCGA	1100
HSV-2		AACCAGCCAC	CGGAGCTCTC	GGTAAAGTAC	CTCAACAACG	AGCGGGCCGA	
Matches		AACCAGCC-C	CGGAGCT-T-	GGT-AA-TAC	CT-AACAACG	A-CGGGCCGA	
HSV-1	1101	ATTTACCAAC	CACCGCCTGA	AGCACGACGT	CGGGTTAGCG	GTTGACCTGT	1150
HSV-2		GTTTAACCAAC	CGCCCCCTGA	AGCACGACGT	CGGGCTGGCG	GTCGATCTCT	
Matches		-TTTA-CAAC	C-CC-CCTGA	AGCACGACGT	CGGG-T-GCG	GT-GA-CT-T	
HSV-1	1151	ACGCCCTGGG	CCAGACGCTG	CTGGAGTTGG	TGGTTAGCGT	GTACGTCGCC	1200
HSV-2		ACGCCCTGGG	GCAGACGCTG	CTGGAGCTGC	TGGTTAGCGT	GTACGTCGCC	
Matches		ACGCCCTGGG	-CAGACGCTG	CTGGAG-TG-	TGGTTAGCGT	GTACGT-GCC	

***Fig. 3D***

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HSV-1	1201	CCGAGCCTGG	GCGTACCCGT	GACCCGGTTT	CCCGGTTACC	AGTATTTTAA	1250
HSV-2		CCGAGCCTGG	GCGTCCCCGT	GACCCGCGTC	CCGGGCTACC	AGTACTTTAA	
Matches		CCGAGCCTGG	GCGT-CCCGT	GACCCG--T-	CC-GG-TACC	AGTA-TTTAA	
HSV-1	1251	CAACCAGCTG	TCGCCGGACT	TCGCCCTGGC	CCTGCTCGCC	TATCGCTGCG	1300
HSV-2		CAACCAGCTC	TCGCCGGACT	TTGCCGTGGC	CCTCCTCGCC	TATCGCCGCG	
Matches		CAACCAGCT-	TCGCCGGACT	T-GCC-TGGC	CCT-CTCGCC	TATCGC-GCG	
HSV-1	1301	TGCTGCACCC	AGCCCTGTTT	GTCAACTCGG	CCGAGACCAA	CACCCACGGC	1350
HSV-2		TTCTGCACCC	CGCCCTCTTT	GTCAACTCGG	CCGAGACCAA	CACCCACGGC	
Matches		T-CTGCACCC	-GCCCT-TTT	GTCAACTCGG	CCGAGACCAA	CACCCACGGC	
HSV-1	1351	CTGGCGTATG	ACGTCCCAGA	GGGCATCCGG	CGCCACCTCC	GCAATCCCAA	1400
HSV-2		CTGGCGTATG	ACGTGCCGGA	GGGCATCCGG	CGCCACCTTC	GCAATCCCAA	
Matches		CTGGCGTATG	ACGT-CC-GA	GGGCATCCGG	CGCCACCT-C	GCAATCCCAA	

**Fig. 3E**

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HSV-1 1401 GATTCGGCGC GCGTTACGG ATCGGTGTAT AAATTACCAG CACACACACA 1450  
 HSV-2 GATTCGGCGC GCGTTACGG AGCAGTGTAT AAATTACCAG CGCACGCCACA  
 Matches GATTCGGCGC GCGTT-ACGG A-C-GTGTAT AAATTACCAG C-CAC-CACA

HSV-1 1451 AGGCGATACT GTCGTCGGTG GCGCTGCCCTC CCGAGCTTAA GCCTCTCCTG 1500  
 HSV-2 AGGCCGTCCT GTCGTCGGTG TCGCTGCCGC CCGAGCTGAG GCCGCTGCTG  
 Matches AGGC--T-CT GTCGTCGGTG -CGCTGCC-C CCGAGCT-A- GCC-CT-CTG

HSV-1 1501 GTGCTGGTGT CCGCCCTGTG TCACACCAAC CCGTGC GCGC GGCACGCGCT 1550  
 HSV-2 GTGCTGGTCT CCGCCCTCTG TCACGCCAAC CCGCCGCGC GCCACTCTCT  
 Matches GTGCTGGT-T CCGCCCT-TG TCAC-CCAAC CCG--CGCGC G-CAC-C-CT

1551

HSV-1 GTCGTGA

HSV-2 GTCGTGA  
 Matches GTCGTGA

**Fig. 3F**

HSV-1 1 ..TACCACAGGTGGTGCTTTGGAAACTTGTGGTCCGCTGCTCCTGTG 48  
 HSV-2 1 ACCACAACAGGTGGTGCTTCGGGGACTTGACGGTCGCCACTCTCCTGCG 50  
 49 AGC...TTGGCTCCCTCCCGGTTTCCTTTGCGTCCCGCCTTCCGGA 93  
 51 AGCCCTCAGCTCTTCGCCCAACCGATTCTCTGTTGCGTTCTGTGCGCCGGT 100  
 94 CCTGCTCTCGCCATCTTCTTTGGCTCTCGGTGCGATTCTGTCAGGCAGCG 143  
 101 GCTGTCTGTGACAGATTGTTGGC.GACTGCCCGGGTGATTCTGTCGGCC 149  
 144 GCCTTGTGGAATCTCGACCCCAACCACTCGCCGGACTCGCCGACGTCCCCT 193  
 150 GGTGCGTCCTTTCGGTCGTACCGCCCAACCCCGCTCCACGGGCCCGCCG 199  
 194 CTCGAGCCCGCCGAAACCCGCCGAAACCCGCCGCTGTGTGAATGGCC 243  
 200 CTGTTCCGTTTCATCGCGTCCGAGCCACCGTCACTTGGTTCCAAATGGCC 249  
 244 AGCCGCCAGCCGCATCTCTCCCGTCGAAGCGCGGCCCGGTTGGGGG 293  
 250 AACCGCCCTGCGCATCCGCCCTCGCCGGAGCGCGGTCTCCGTCCGAACG 299  
 294 ACAGGAGCCCGCGGCCCAAGCGCAGCCACCCAGGGGAGGCCCGCGGG 343  
 300 ACAGGAACCCCGGAGCCCGAGGTGCGCCCCCCCCTGG..... 335

**Fig. 4A**

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344 CCCCTCTCGCCCAACGGCCACACAGTGTACTGCCAGCGAGTCAATGGCGTG 393  
|||||  
336 .....CGGCGACCAACGTGTTTTCAGGAAAGTCAGCGCGTG 372  
394 ATGGTGCTTTCGACACAAGACGCCCGGGTCCGGTCCCTACCGCATCAGCGA 443  
|||||  
373 ATGGTGCTTTCAGCGATCCCCCGCGCCCGCGCTACCGCATTAGCGA 422  
444 TAGCAACTTTGTCCAATGTGGTTCCAACCTGCACCATGATCATCGACGGAG 493  
|||||  
423 CAGCAGCTTTGTTCAATGCGGCTCCAACTGCAGTATGATAATCGACGGAG 472  
494 ACGTGGTGCGCGGGCGCCCCCAGGACCCGGGGCGCGGCGATCCCCCGCT 543  
|||||  
473 ACGTGGCGCGCGGTCAATTGCGTGACCTCGAGGGCGCTACGTCCACCGGC 522  
544 CCCTTCGTTGCGGTGACAAACATCGGAGCCGGCAGCGACGGCGGACCGC 593  
|||||  
523 GCCTTCGTCGCGATCTCAAACGTGCGAGCCGCGGGGATGGCCGAACCGC 572  
594 CGTCGTGGCATTCGGGGGAACCCACGTCTCGCTCGGCGGGACGTCTACCG 643  
|||||  
573 CGTCGTGGCGCTCGGCGGAACCTCGGGCCCGTCCGCGGACTACATCCGTGG 622

*Fig. 4B*

644 GTACCCAGACGGCC...GACGTCCCCACCGAGGCCCTTGGGGGCCCC... 687  
 623 GGACCCAGACGTCCGGGAGTTCTCTCCACGGGAACCCAGGACCCCGAA 672  
 688 .....CCTCCTCCTCCCGCTTCACTGGGTGGCGCTGTTGTTTC 728  
 673 CCCCAGGACCCAGGCTGTCCCCCGCCCTCTCCCTTCCATG 722  
 729 CTGTCCGACACACGGCGCGCTCTGCGGTATTCGGGGGAGGGGATC 778  
 723 GGGCCACGAGTGCTGCGCCCGTCGCGATGCCAGGGCGCGCGAGAAG 772  
 779 CAGTCGGCCCCGGGAGTTCTCTCGGACGACCGGTCTCGGATTCGAC 828  
 773 ACGTCGGGGCGCGGAGTCATGTGTCAGACGGCCCGTCGTCGACTCCGAA 822  
 829 TCGGATGACTCGGA.....GGACACGGACTCGGAGAC 860  
 823 ACGGAGACTCGGACTCCTCGGACGAGGATACGGGCTCGGGTTCGGAGAC 872  
 861 GCTGTACACGCCCTCCTCGGACGTGTCCGGCGGGGCCACGTACGACGAC 910  
 873 GCTGTCTCGATCCTCTTCGATCTGGGCCCGCAGGGCGACTGACGACGATG 922  
 911 CCCTTGACTCCGATTCGTCAATCGGATGACTCCCTGCAGATAGATGCCCC 960  
 923 ACAGCGACTCCGACTCGGGTCCGACGACTCCGTGACGCCCGACGTTGTC 972

**Fig. 4C**

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[illegible]

**Fig. 4D**

11287	CGAGGAAACCAAGCGTGTCTCCCGCCACGAGACATTCGGCAGCCCCCCTCGCC	1336
11314	CGAGGAGAGCAAGCGGTGCCCCCACGAACCTTCGGCAGCGCCCCCGCC	1363
11337	TCACGGAGGACGACTTTGGGCTTCTCAACTACGCGCTCGTGGAGATGCAG	1386
11364	TCACGGAGGACGACTTTGGGCTCCTGAACCTACGCGCTCGTGAGATGCCA	1413
11387	CGCCTGTGTCTGGACGTTCCCTCCGGTCCCGCCGAACGCATACATGCCCTA	1436
11414	CGCCTGTGCCTGGACCTTCCCCCGGTCCCCCAACGCATACACGCCCTA	1463
11437	TTATCTCAGGGAGTATGTGACGCGGCTGGTCAACGGGTTCAAGCCGCTGG	1486
11464	TCATCTGAGGGAGTATGCGACGCGGCTGGTTAACGGGTTCAAACCCCTGG	1513
11487	TGAGCCGGTCCGCTCGCCTTTACCGCATCCTGGGGGTTCTGTGTCACCTG	1536
11514	TGCGGCGGTCCGCCCGCCTGTATCGCATCCTGGGGATTCTGTTCAACCTG	1563
11537	CGGATCCGGACCCGGGAGGCCCTCCTTTGAGGAGTGGCTGCGATCCAAGGA	1586
11564	CGCATCCGTACCCGGGAGGCCCTCCTTTGAGGAATGGATGCGCTCCAAGGA	1613
11587	AGTGGCCCTGGATTTTGGCCTGACGGAAAGGCTTCGCGAGCACGAAGCCC	1636
11614	GGTGGACCTGGACTTCGGGCTGACCGAAAGGCTTCGCGAACACGAGGCC	1663

**Fig. 4E**



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1637 AGCTGGTGATCCTGGCCAGGCTCTGGACCATACGACTGTCTGATCCAC 1686  
|||||  
1664 AGCTAATGATCCTGGCCAGGCCCTGAACCCCTACGACTGTCTGATCCAC 1713  
|||||  
1687 AGCACACCGCACACGCTGGTCGAGCGGGGCTGCAATCGGCCCTGAAGTA 1736  
|||||  
1714 AGCACCCCGAACAACGCTCGTCGAGCGGGGCTGCAGTCGGCGCTGAAGTA 1763  
|||||  
1737 TGAGGAGTTTACCTAAAGCGTTTGGCGGGCCTACTACATGGAGTCCGCTCT 1786  
|||||  
1764 CGAAGAGTTTACCTCAAGCGCTTCGGCGGGCCTACATGGAGTCCGCTCT 1813  
|||||  
1787 TCCAGATGTACACCCGCATCGCCGGCTTTTGGCCCTGCCGGCCACGCCG 1836  
|||||  
1814 TCCAGATGTACACCCGCATCGCCGGGTTCCTGGCGTGCCGGCGACCCGC 1863  
|||||  
1837 GGCATGCGCCACATCGCCCTGGGGCGAGAGGGGTCGTGGTGGGAAATGTT 1886  
|||||  
1864 GGCATGCGCCACATCGCCCTGGGGCGACAGGGGTCGTGGTGGGAAATGTT 1913  
|||||  
1887 CAAGTCTCTTTTCCACCGCCTCTACGACCCACAGATCGTACCGTCGACCC 1936  
|||||  
1914 CAAGTCTCTTTTCCACCGCCTCTACGACCCACAGATCGTGGCGTCCACCC 1963  
|||||  
1937 CCGCCATGCTGAACCTGGGGACCCGCAACTACTACACCTCCAGCTGCTAC 1986  
|||||  
1964 CCGCCATGCTGAACCTCGGAACCCGCAACTACTACACCTCCAGCTGCTAC 2013  
|||||

***Fig. 4F***

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1987 CTGGTAAACCCCCAGGCCACCAACAAGCGACCCCTGCGGGCCATCAC . 2036  
|||  
2014 CTGGTAAACCCCCAGGCCACCACTAACAGGCCACCCCTCGGGCCATCAC 2063  
|||  
2037 CAGCAACGTGAGTGCCATCCTCGCCCCGCAACGGGGGCATCGGGCTATGCG . 2086  
|||  
2064 CGGCAACGTGAGGCCATCCTCGCCCCGCAACGGGGGCATCGGGCTGTGCA 2113  
|||  
2087 TGCAGGCGTTTAAAGACTCCGGCCCCCGGACCGCCAGCGTCATGCCGCC . 2136  
|||  
2114 TGCAGGCGTTCAACGACGCCAGCCCCCGGACCGCCAGCATCATGCCGCC 2163  
|||  
2137 CTCAAGGTCCTTGACTCGCTGCTGGCGGCGCACAAACAAGAGCGCGCG . 2186  
|||  
2164 CTGAAGGTCCTGGACTCCCTGCTGGCGGCGCACAAACAAGAGCACGCG 221  
|||  
2187 TCCGACCGGCGCGTGCGTGACCTGGAGCCGTGGCACACCGACGTGCGGG . 2236  
|||  
2214 CCCACCGGGCGTGCGTGACCTGGAACCCCTGGCACAGCGACGTTGCGG 2263  
|||  
2237 CCGTGCTCCGGATGAAGGGGTCTCTCGCCGCGGAAGAGGCCACGCGCTGC . 2286  
|||  
2264 CCGTGCTCAGAAATGAAGGGCGTCTCTCGCCGCGGAGAGGCCACGCGCTGC 2313  
|||  
2287 GACAATATCTTCAGCGCCCTCTGGATGCCAGACCTGTTTTCAGCGCCT . 2336  
|||  
2314 GACAACATCTTCAGCGCCCTCTGGATGCCGAGACCTGTTCTTCAAGCGCCT 2363  
|||

***Fig. 4G***

2337	GATCGCCACCTGGACGGGAGAGAAACGTCAATGGACCCCTGTTTCGACC	2386
2364	GATCCGCCACCTCGACGGCGAGAAAACGTCACTGGTCCCTGTTTCGACC	2413
2387	GGGACACCAAGCATGTCGCTCGCCGACTTTCACGGGGAGGAGTTCGAGAAG	2436
2414	GGGACACCAAGCATGTCGCTCGCCGACTTTCACGGCGAGGAGTTCGAGAAG	2463
2437	CTCTACCAGCACCTCGAGGTCATGGGGTTCGGCGAGCAGATACCCATCCA	2486
2464	CTGTACGAGCACCTCGAGGCCATGGGGTTCGGCGAAACGATCCCCATCCA	2513
2487	GGAGCTGGCCCTATGGCATTTGTGCGCAGTGGGCCACGACCGGAGCCCCCT	2536
2514	GGACCTGGCGGTACGCCATCGTGGCGCAGCGCGGCCACCAACGGGAGCCCCCT	2563
2537	TCGTCAATGTTCAAAGACGCGGTGAACCGCCACTACATCTACGACACCCAG	2586
2564	TCATCATGTTTAAGGACGGCGTTAAACCGCCACTACATCTACGACACGCAA	2613
2587	GGGGCGGCCATCGCCGGCTCCAACCTCTGCACCGAGATCGTCCATCCGGC	2636
2614	GGGGCGGCCATTGCCGGCTCCAACCTCTGCACGGAGATCGTCCACCCGTC	2663
2637	CTCCAAGCGATCCAGTGGGGTCTGCCAACCTGGGAAGCGTGAATCTGGCCC	2686
2664	CTCCAAAACGCTCCAGCGGGGTCTGCCAACCTGGGCAGCGTGAATCTGGCCC	2713

**Fig. 4H**

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2687 GATGCGTCTCCAGGCAGACGTTTGA<sup>.</sup>CTTTGGGCGGCTCCGCGACGCCGTG<sup>.</sup> 2736  
|||||  
2714 GATGCGTCTCCCGGCGGACGTTTCGATTTTGGCATGCTCCGCGACGCCGTG<sup>.</sup> 2763  
|||||  
2737 CAGGCGTGCGTGCTGATGGTGAACATCATGATCGACAGCACGCTACAACC<sup>.</sup> 2786  
|||||  
2764 CAGGCGTGCGTGCTAATGGTTAATATCATGATAGACAGCACGCTGCAGCC<sup>.</sup> 2813  
|||||  
2787 CACGCCCCAGTGCACCCCGCGGCAACGACAACCTGCGGTCCATGGGAATCG<sup>.</sup> 2836  
|||||  
2814 GACGCCCCAGTGCGCCCGCGGCCACGACAACCTGCGGTCCATGGGCATTG<sup>.</sup> 2863  
|||||  
2837 GCATGCAGGGCCTGCACACGGCCTGCCTGAAGCTGGGGCTGGATCTGGAG<sup>.</sup> 2886  
|||||  
2864 GCATGCAGGGCCTGCACACGGCGTGCTGAAGATGGCCCTGGATCTGGAG<sup>.</sup> 2913  
|||||  
2887 TCTGCCGAATTTCAGGACCTGAACAAACACATCGCCGAGGTGATGCTGCT<sup>.</sup> 2936  
|||||  
2914 TCGGCCGAGTTCGGGGACCTGAACACACACATCGCCGAGGTGATGCTGCT<sup>.</sup> 2963  
|||||  
2937 GTCGGCGATGAAGACCAAGCAACGCGCTGTGCGTTCGCGGGGCCGTCCCT<sup>.</sup> 2986  
|||||  
2964 CGCGGCCATGAAGACCAAGTAACGCGCTGTGCGTTCGCGGGGCCGTCCCT<sup>.</sup> 3013  
|||||  
2987 TCAACCACTTTAAGCGCAGCATGTATCGCGCCCGCGCTTTCACCTGGGAG<sup>.</sup> 3036  
|||||  
3014 TCAGCCACTTTAAGCGCAGCATGTACCGGGCCCGCGCTTTCACCTGGGAG<sup>.</sup> 3063  
|||||

***Fig. 4I***



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[illegible]

**Fig. 4K**

3637 AGCTGCCGCGCTGTGA 3651  
 3664 AGCTGCCGCGCTGTAA 3678

```

HSV-1 1 GTACTACTGCAAGGTTTCGCAAGCGGACCAACAGCGGGTGTTGCGCGGCG 50
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
HSV-2 1 ..ACTACTGCAAGGTTTCGCAAGCGGACCAACAGCGGGTGCTTTGGCGGCG 48
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      51 ACGACAAACATCGTCTGCACAAAGCTGCGGCTGTAAAGCAACA...GCGCTC 97
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      49 ACGACAAACATGCTCTGCAC.GGCTGCGGCGCTGTGACCGACAAACCCCTC 97
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      98 CGATCGGGTCAAGCGTCTCGTCTCGGTCCCGCATATCG..... 135
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      98 CGCGCCAGGCCCGCGCCACTGTCTGTCGCGCGTCCACGCGCTCCCCCGCT 147
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      136 .....CQATGGATCCCGCGCGTCTCCCCCGCGAGCACCGACCCCT 175
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      148 GCCATGATTCGCGGCCCGCGCCCTCTCCCCCGCTCTGACGGGCCATAC 197
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      176 AGATACCCACGCGTCCGGGCGCGGCGGCCCGGATTCGGGTGTGCCCA 225
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      198 GGGCCATAGCGGACCGGACCTAGCGATCCAGATTCCAAAGTGCCCGG 247
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      226 CCCCCGAGGGTACTTCTACACCTCCCAGTGCCCCGACATCAACCACCTT 275
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      248 ACCCCGAGAGGTACTTCTACACCTCCCAGTGTCCTCCGACATTAAACCCTG 297
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      276 CGCTCCCTCAGCATCCTGAACCGCTGGCTGGAGACCGAGCTCGTGTTCGT 325
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      298 CGCTCCCTCAGCATCCTTAACCGCTGGCTGGAAACCGAGCTTGTTTTCGT 347
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

**Fig. 5A**

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326 GGGGACGAGGAGCGTCTCCAAGCTCTCCGAGGGCGAGCTCGGCTTCT 375  
|||||  
348 GGGGACGAGGAGCGTCTCCAAGCTTTCCGAGGGCGAGCTCAGCTTTT 397  
|||||  
376 ACCGCTTCTGTGTCCTTCCCTGTCTGGCGCGGACGACCTGGTGACGGAA 425  
|||||  
398 ACCGCTTCTTCCGCTTTCCGCTGTCTGGCGCGGACGACCTGGTTACGGAA 447  
|||||  
426 AACCTGGCGGCCCTCTCCGGCCCTCTTCGAACAGAGACATTCTTCACTA 475  
|||||  
448 AACCTGGCGGCCCTCTCCGGCCCTGTTTGAGCAGAGGACATTCTCCACTA 497  
|||||  
476 CTACGTGGAGCAGGAATGCATCGAGGTCGTCCACTCGCGCGTCTACAACA 525  
|||||  
498 CTACGTGGAGCAGGAATGCATCGAAGTCGCACACTCGCGCGTGTACAACA 547  
|||||  
526 TCATCCAGCTGGTGCTCTTTCAACAACAACGACCGCGCGCCGCTAT 575  
|||||  
548 TCATCCAGCTGGTGCTTTTCCACAACAACGACCGCGCGCGGAGTAC 597  
|||||  
576 GTGGCCCGCACCATCAACCAACCGGCCATTTCGCGTCAAGGTGGACTGGCT 625  
|||||  
598 GTGGCCCGCACCATCAACCAACCGGCCATCCGCGCCAAGGTGGACTGGCT 647  
|||||  
626 GGAGGCGCGGGTGCGGGGAATGCGACTCGATCCCGGAGAAGTTCCTCA 675  
|||||  
648 GGAAGCGCGGGTGCGGGGAATGCGCCTCCGTTCCGGAAAAGTTCATTCTCA 697  
|||||

***Fig. 5B***



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676 TGATCCCTCATCGAGGGCGTCTTTTGTGCGCCTCGTTGCGCGCCATCGCG 725  
|||||  
698 TGATCCCTCATCGAGGGCATCTTTTGTGCGCCTCGTTGCGCGCCATCGCG 747  
|||||  
726 TACCTGCGCACCAACACCTCCTGCGGGTCACTGCCAGTCGAACGACCT 775  
|||||  
748 TACCTTGCACCAACACCTTCTGCGGGTCACTGCCAGTCAACGACCT 797  
|||||  
776 CATCAGCCGCGACGAGGCCGTGCATACGACAGCCCTCGTGCTACATCTACA 825  
|||||  
798 CATCAGCCGCGACGAGGCCGTGCACACGACGCGCCTCGTGTTACATCTACA 847  
|||||  
826 ACAACTACCTCGGGGGCCACGCCAAGCCGAGCGCGCGGTGTACCGG 875  
|||||  
848 ACAACTACCTGGGGGGCACGCCAAGCCCCGCCGCGCGGTGTACGGG 897  
|||||  
876 CTGTTTCGGGAGGCGGTGGATATCGAGATCGGGTTTCATCCGATCCCAGGC 925  
|||||  
898 CTGTTCCGCGAGGCGGTGAGATCGAGATCGGATTTATCCGATCCCAGGC 947  
|||||  
926 CCGACGGACAGCTCTATCCTGAGTCCGGGGCCCTGGCGGCCATCGAGA 975  
|||||  
948 GCCGACGGACAGCCATATCCTGAGCCCCGGCGCGCTGGCGGCCATCGAAA 997  
|||||  
976 ACTACGTGCGATTACGCGGGATCGCCTGCTGGGCCCTGATCCATATGCAG 1025  
|||||  
998 ACTACGTGCGATTACGCGGGATCGCCTGTTGGGCCCTTATCCACATGAAG 1047  
|||||

Fig. 5C



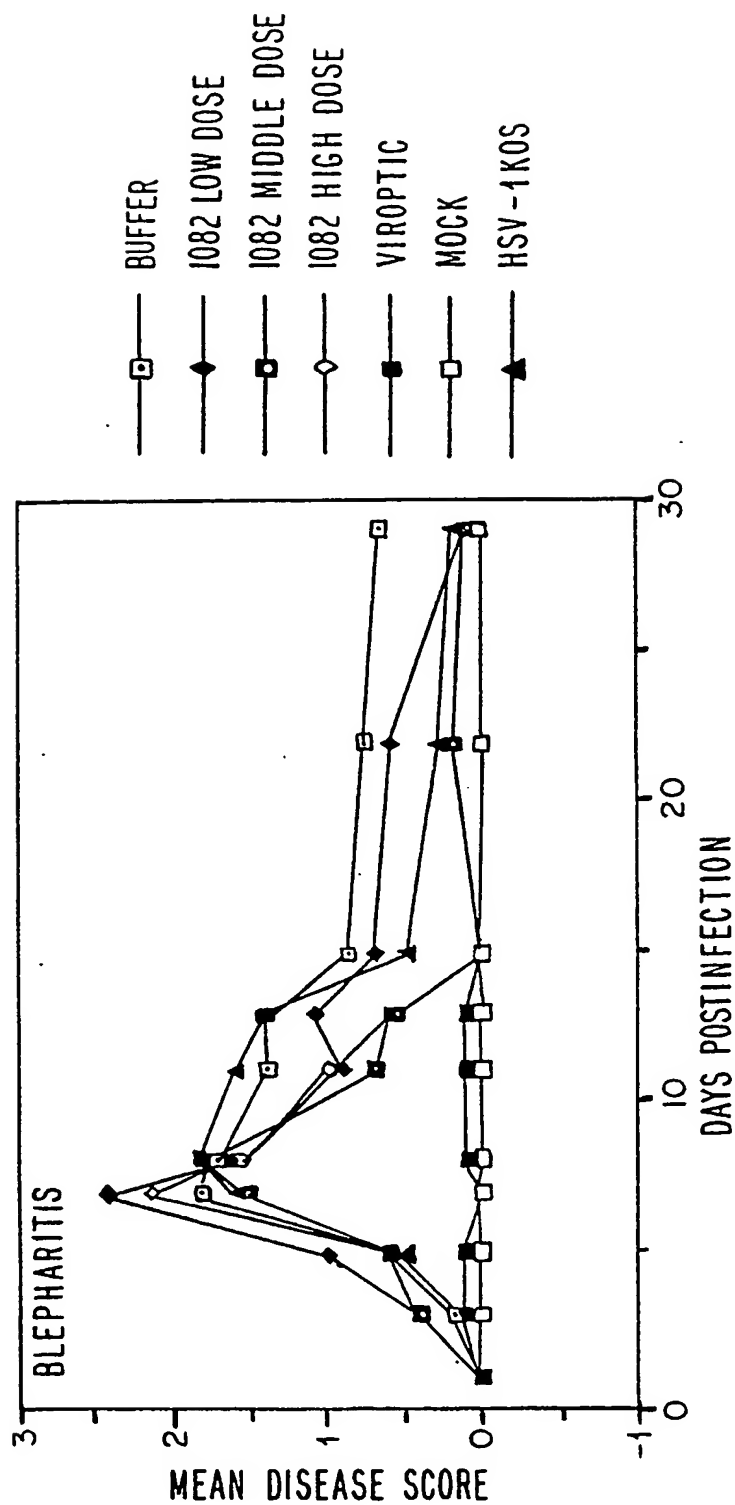
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HSV-1	VZV	EBV
UL5 (6133-3485)	55 (95996-98641)	BBLF4 (114259-111830)
UL8 (11478-9226)	52 (90493-92808)	BBRF1 (114204-116045)
UL9 (14261-11706)	51 (87881-90388)	BBRF2 (116045-119137)
UL13 (19504-17948)	47 (83168-84700)	BGLF4 (123613-122325)
UL29 (53053-49463)	29 (50857-54471)	BALF2 (164770-161384)
UL30 (53807-57514)	28 (50636-47052)	BALF5 (156746-153701)
UL39 (77444-80857)	19 (28845-26518)	BORF2 (76407-78887)
UL40 (80926-81948)	18 (26493-25573)	BaRF1 (78900-79808)
UL42 (84113-85579)	16 (23794-22568)	BMRF1 (79899-81113)
UL52 (100048-103224)	6 (8577-5326)	BSLF1 (86879-84257)

Fig. 6aFig. 6bFig. 6c

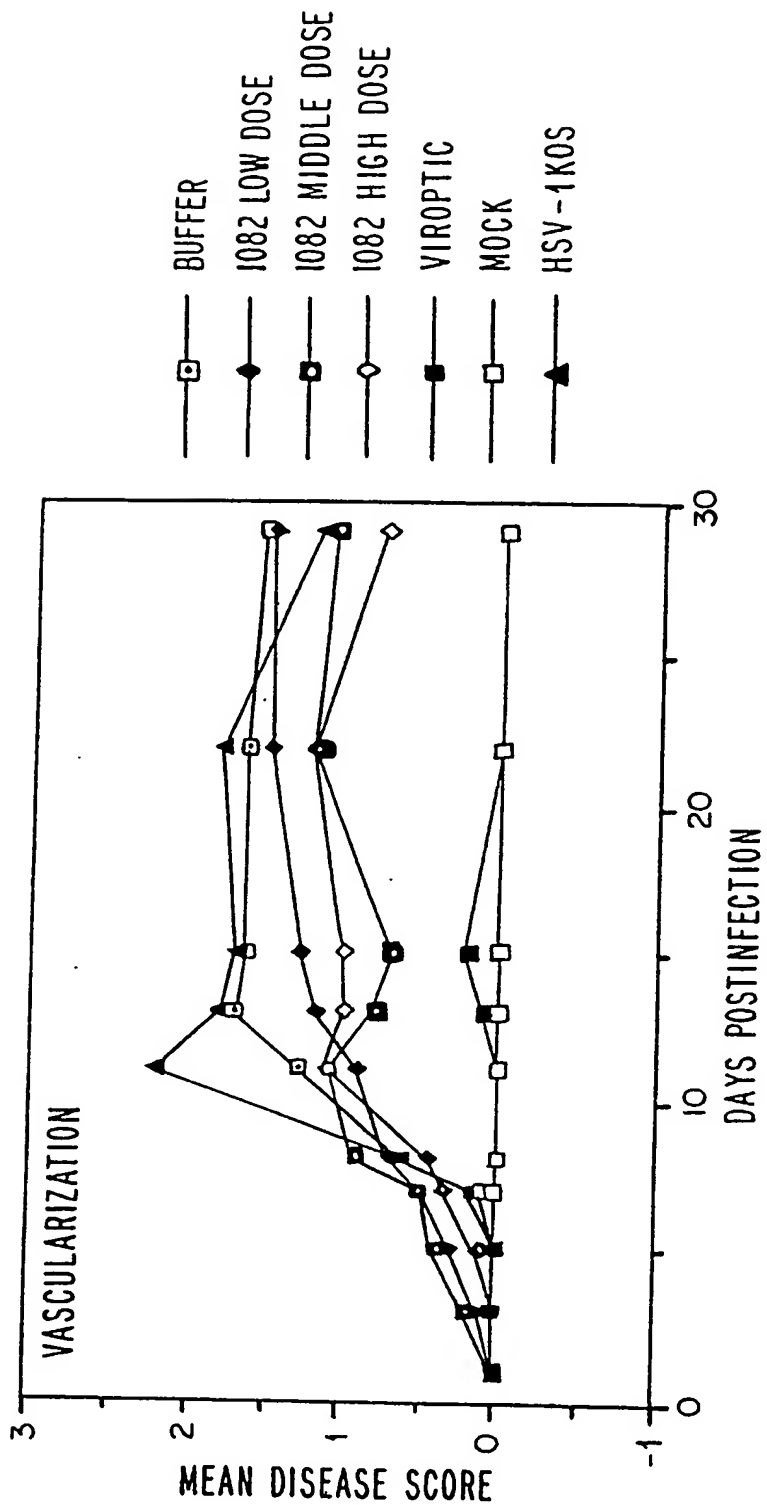
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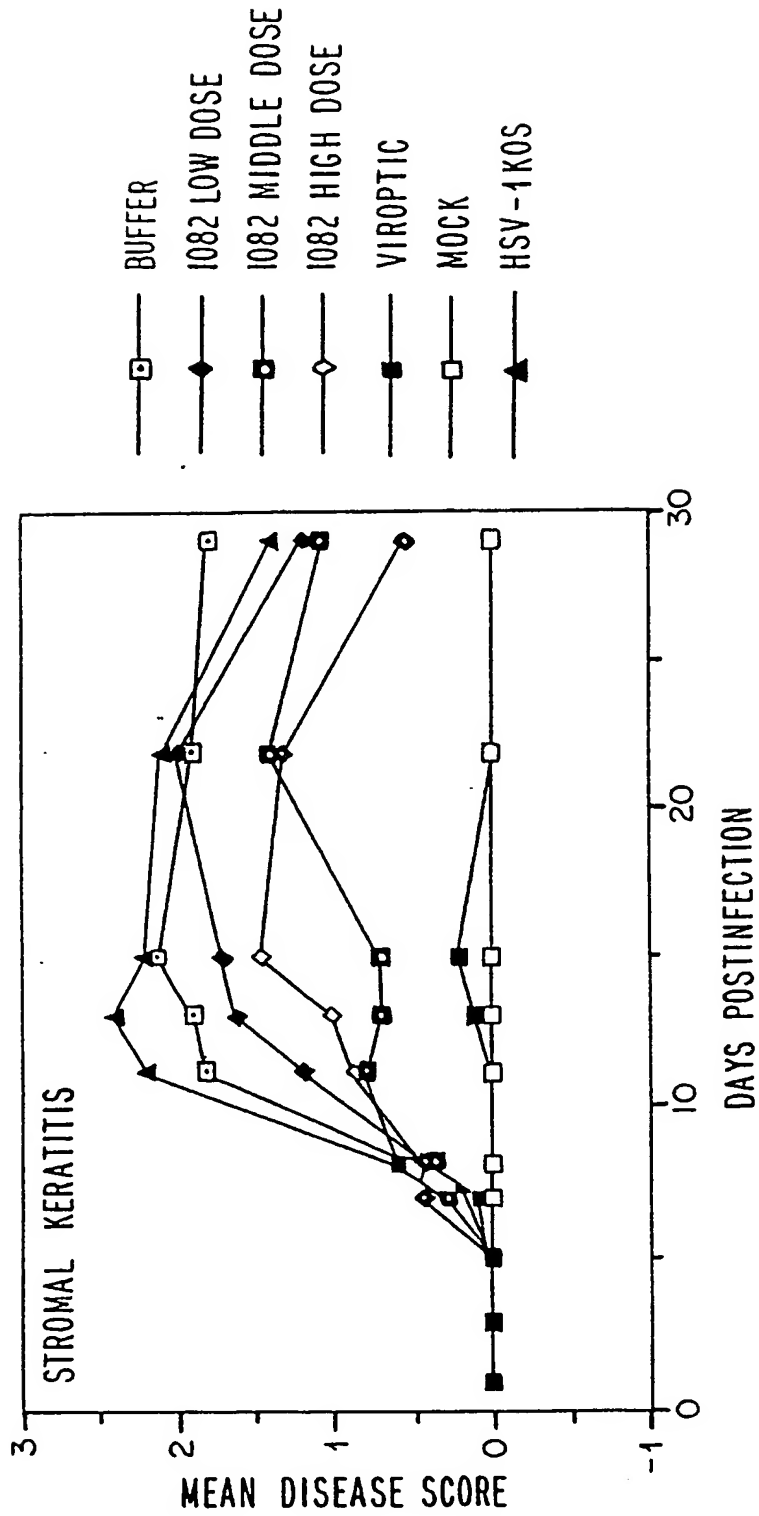
*Fig. 7a*

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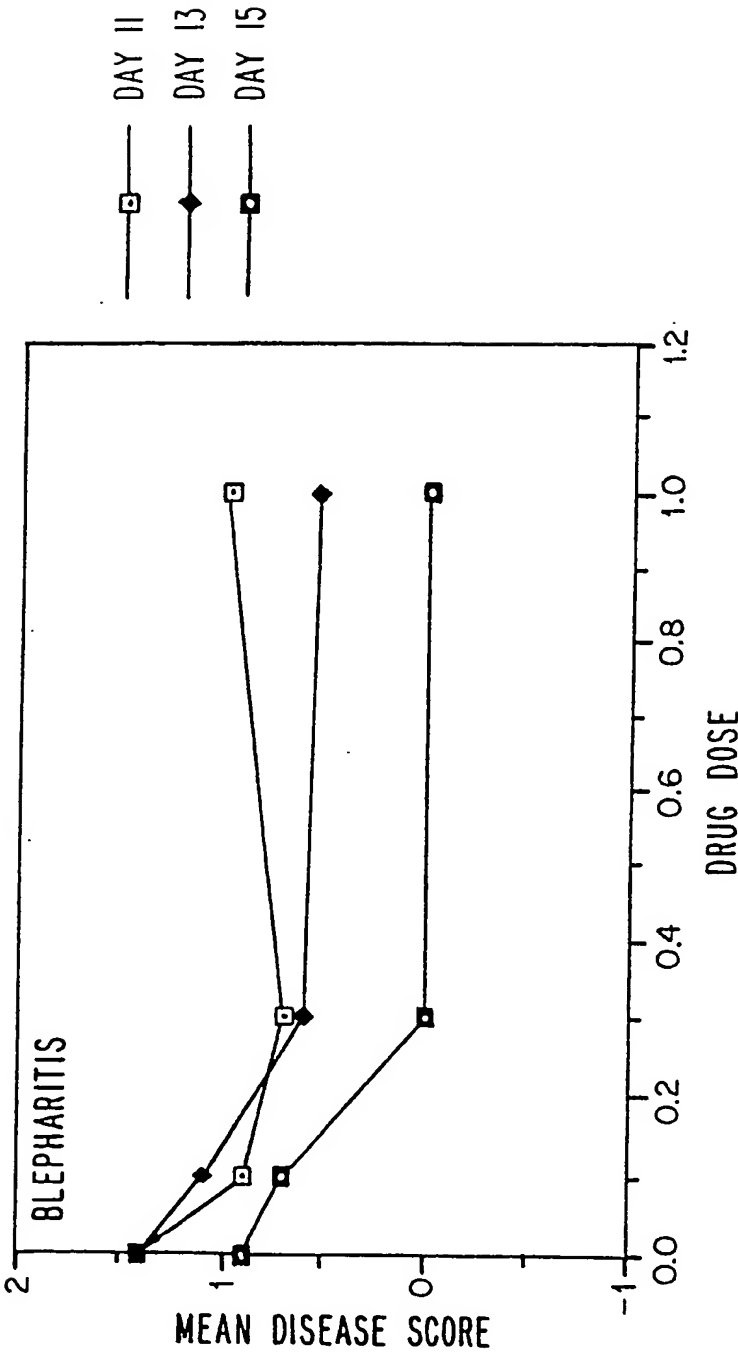
*Fig. 7b*

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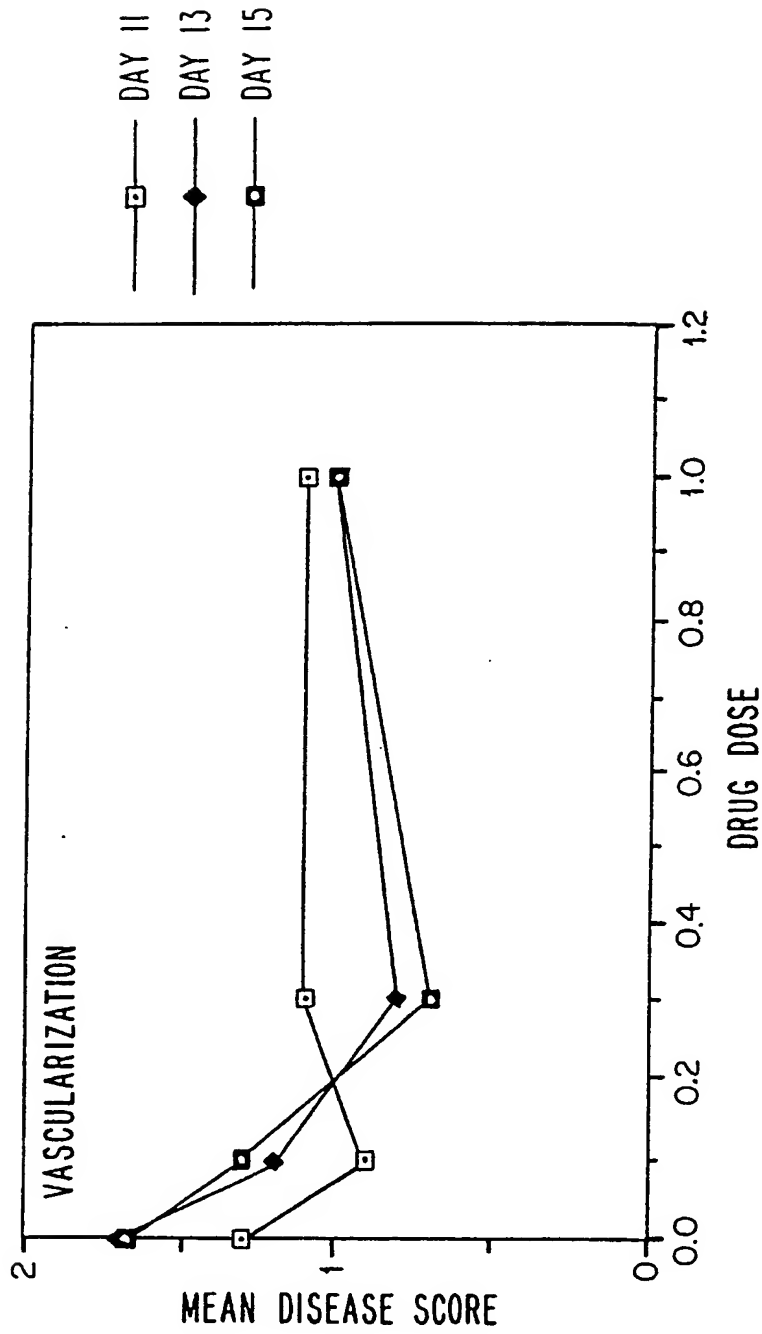
**Fig. 7c**

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*Fig. 8a*

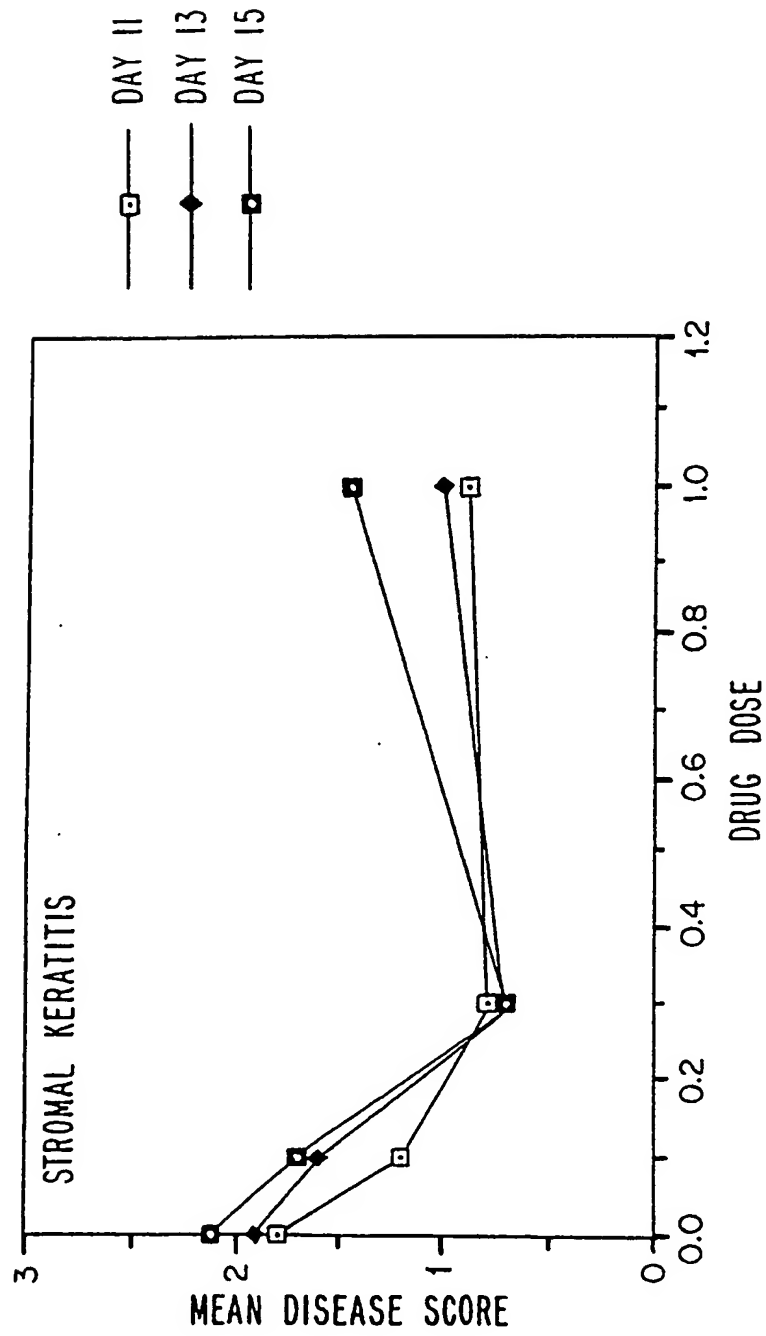
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**Fig. 8b**

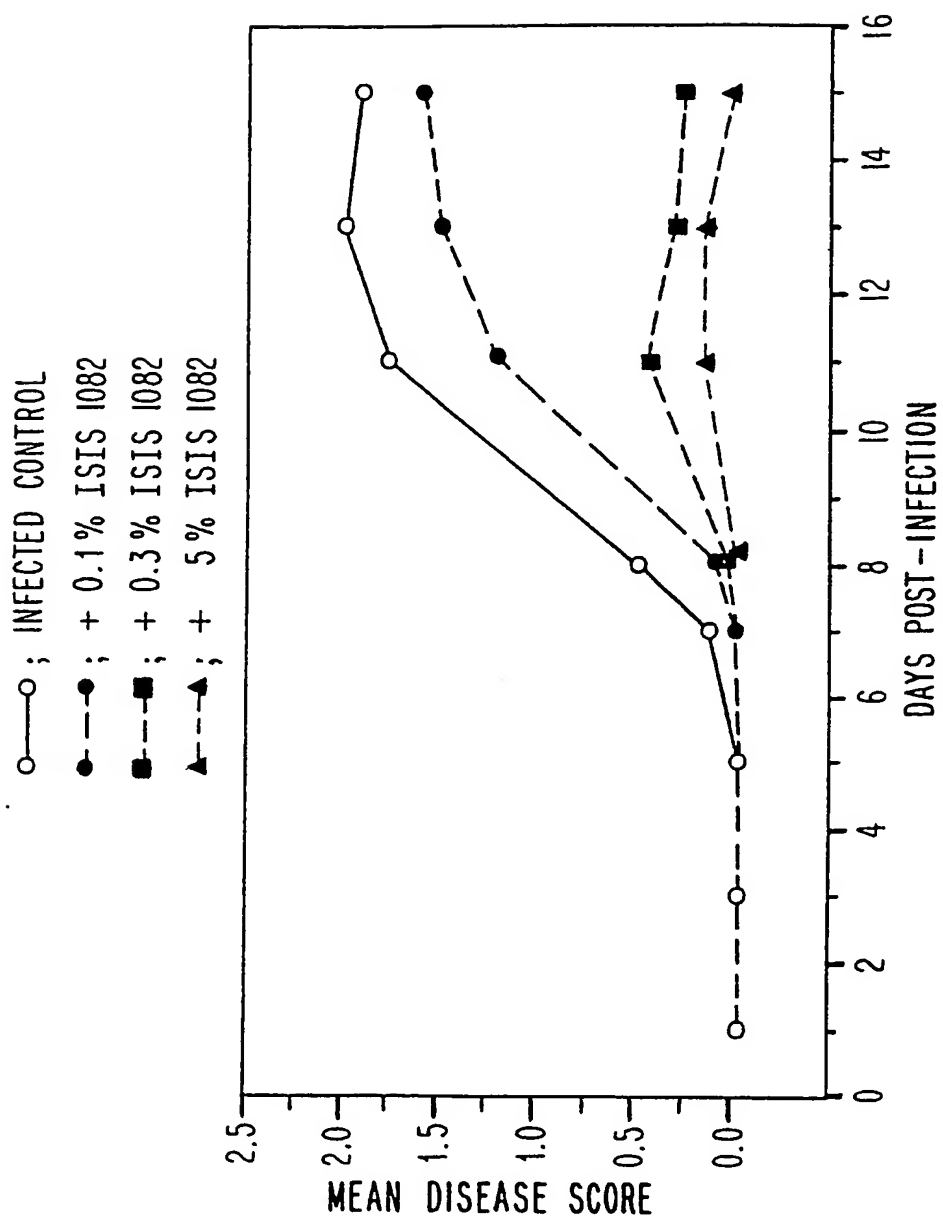


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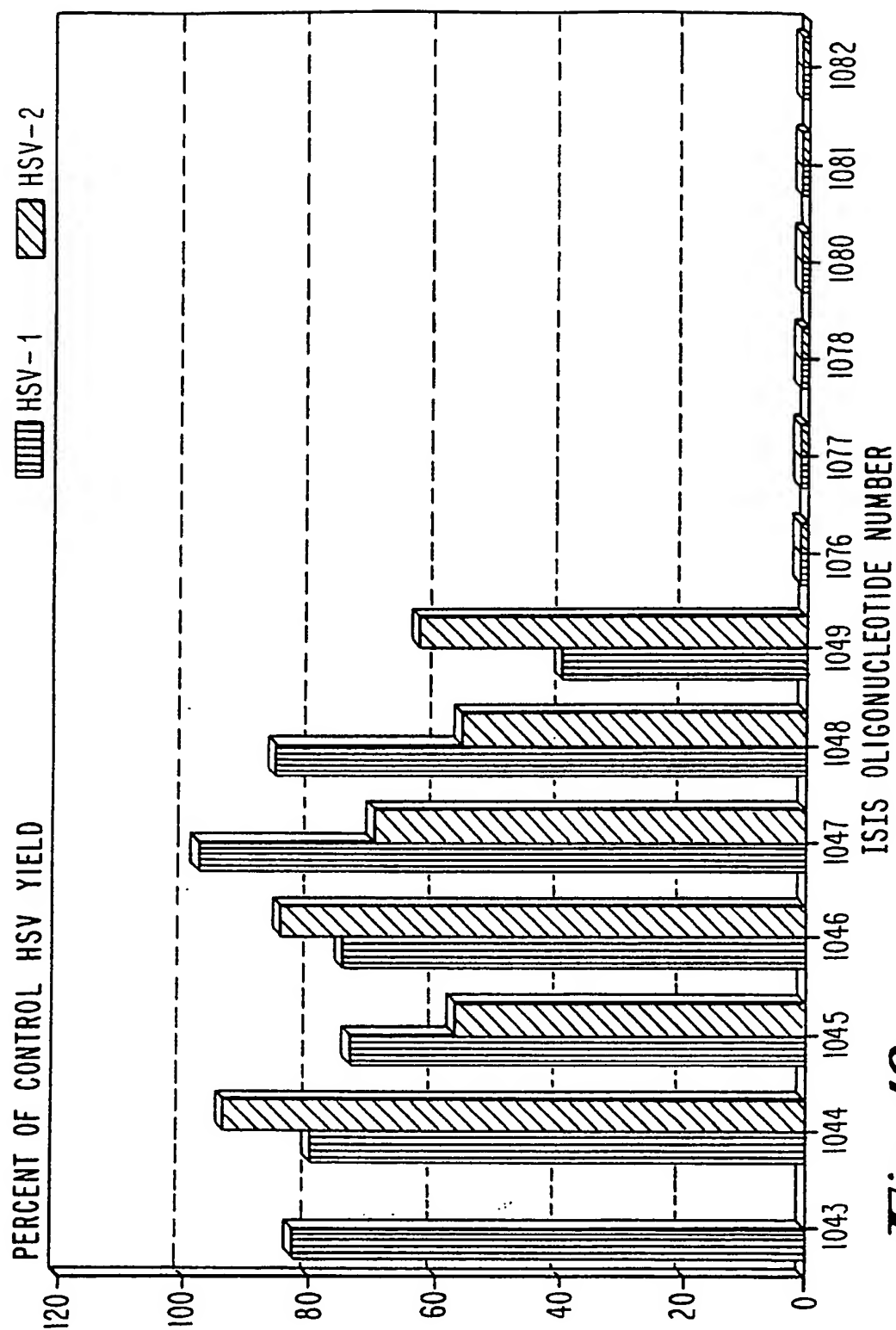
**Fig. 8c**

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*Fig. 9*

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**Fig. 10**

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FIG.IIA

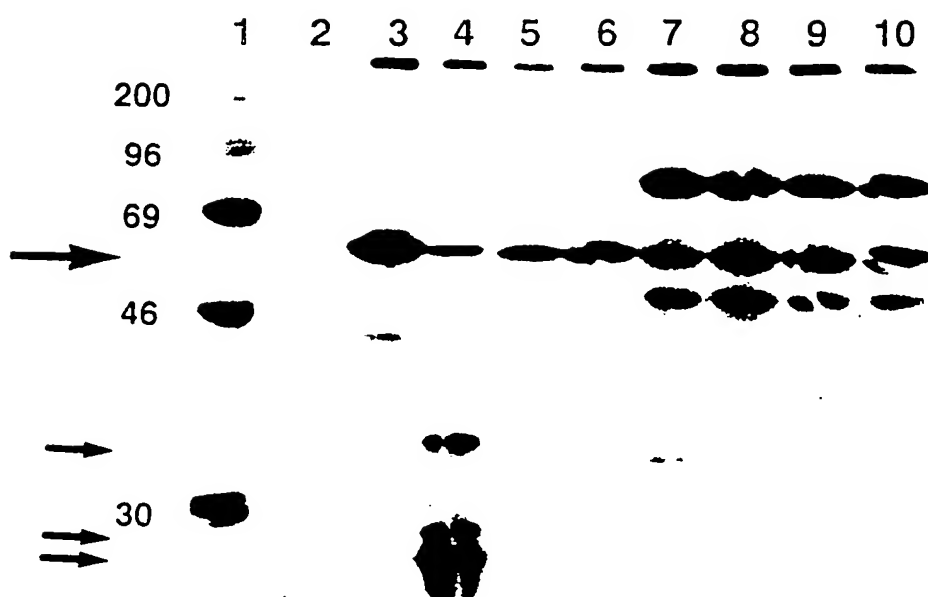
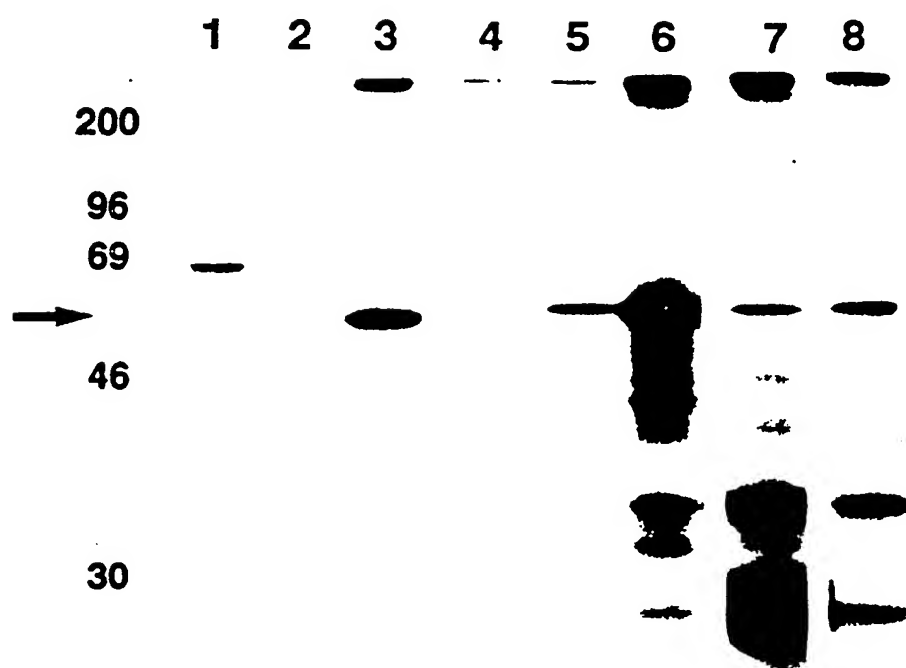
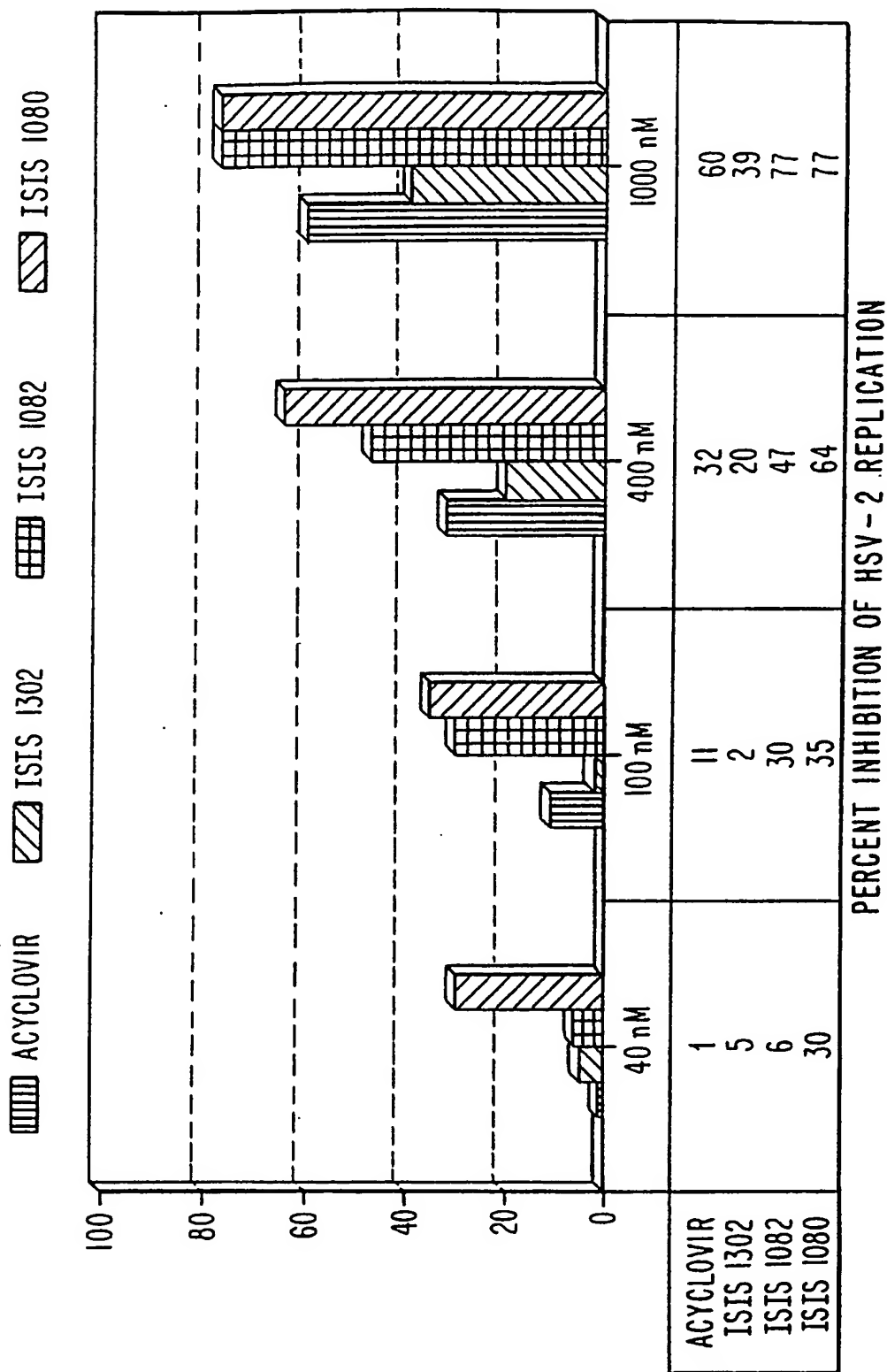


FIG.IIB

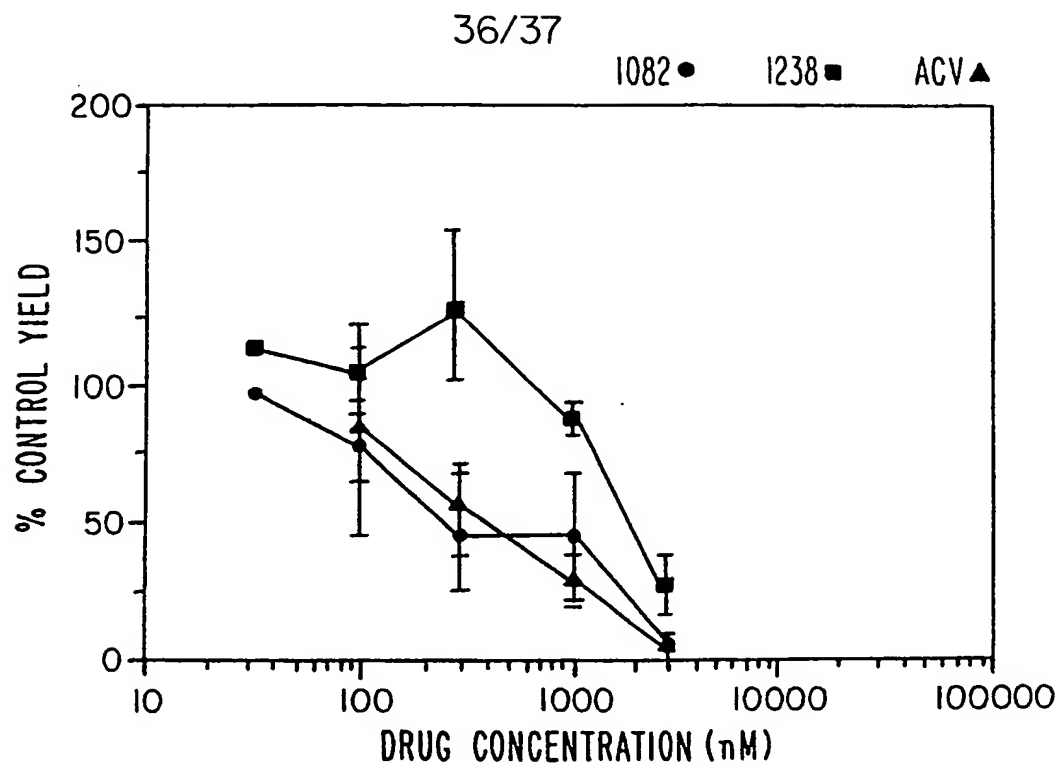


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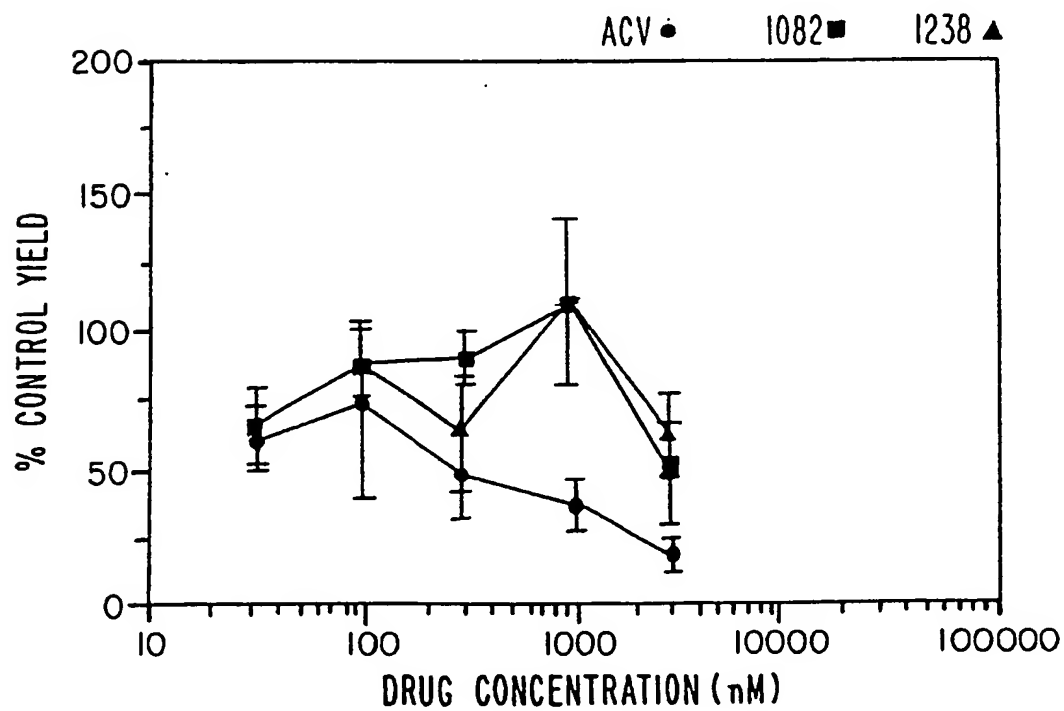
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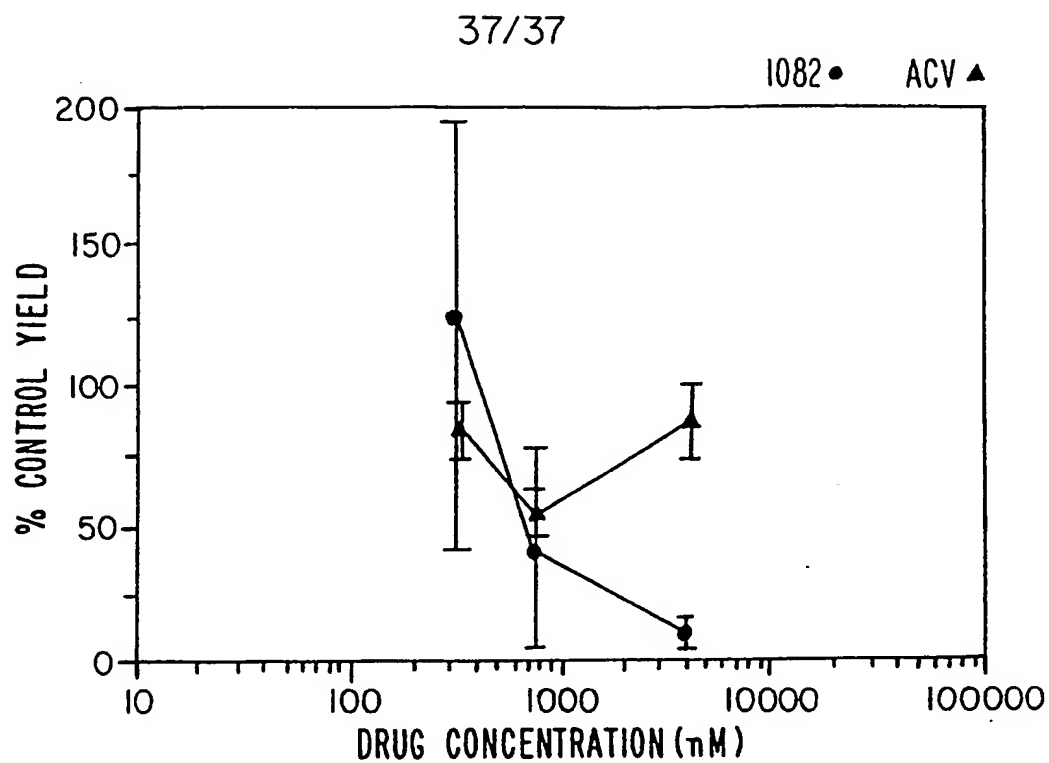
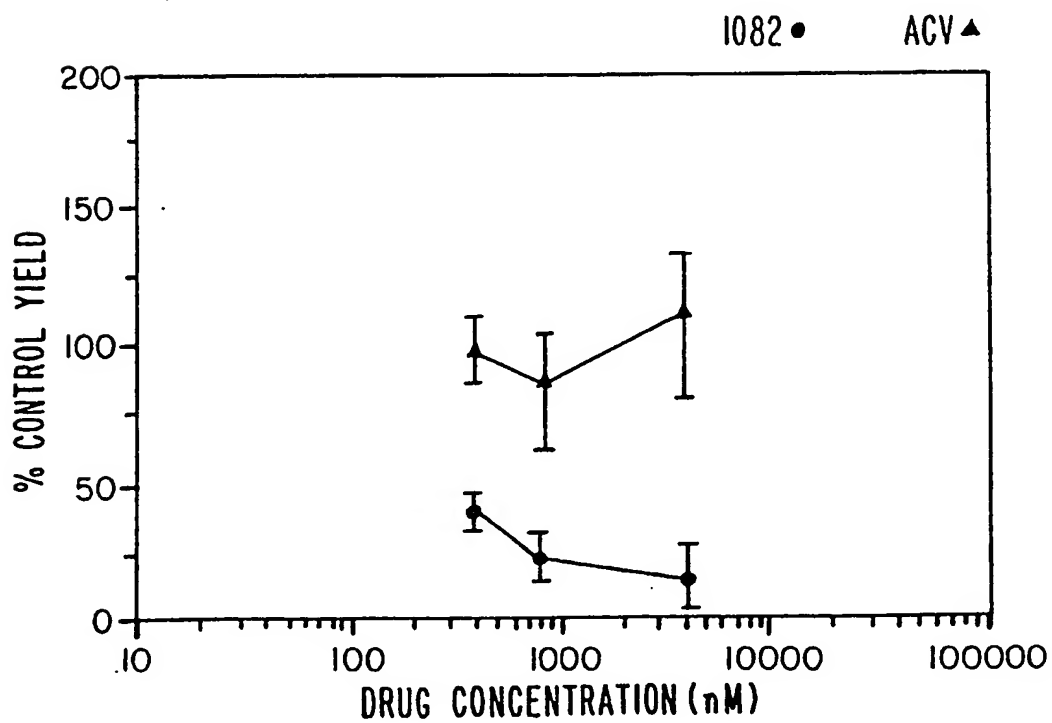
**Fig. 12**



***Fig. 13***

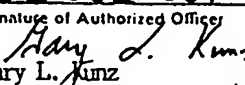


***Fig. 14***

***Fig. 15A******Fig. 15B***

# INTERNATIONAL SEARCH REPORT

International Application No. PCT/US91/01327

<b>I. CLASSIFICATION ( )</b>		<b>SUBJECT MATTER</b> (if several classification symbols apply, indicate all) *	
According to International Patent Classification (IPC) or to both National Classification and IPC			
INT. CL.(5): A61K 31/70; C12Q 1/68; C07H 21/02, 21/04; A61K 48/00			
U.S. CL.: 536/27; 435/6, 33; 514/43			
<b>II. FIELDS SEARCHED</b>			
Minimum Documentation Searched <sup>7</sup>			
Classification System	Classification Symbols		
U.S. CL	536/27; 435/6,33; 935/33; 514/43		
Documentation Searched other than Minimum Documentation to the Extent that such Documents are Included in the Fields Searched <sup>8</sup>			
<b>III. DOCUMENTS CONSIDERED TO BE RELEVANT <sup>9</sup></b>			
Category <sup>9</sup>	Citation of Document, <sup>11</sup> with indication, where appropriate, of the relevant passages <sup>12</sup>	Relevant to Claim No. <sup>13</sup>	
Y	US,A, 4,806,463 (GOODCHILD ET AL) 21 February 1989, See claims 1-12.	1-26	
Y	Nucleosides and Nucleotides, Vol. 8, No. 5 & 6, issued 1989, CERUZZI ET AL, "THE INTRACELLULAR AND EXTRACELLULAR FATE of Oligodeoxyribonucleotides in Tissue Culture Systems," See pages 815-818.	1-26	
Y	Proc. Natl. Acad. Sci, Vol 84, issued November 1987, MATSUKURA ET AL., "Phosphorothioate analogs of oligonucleotides: Inhibitors of Replication and Cytopathic Effects of Human Immunodeficiency virus," see pages 7706-7710.	1-26	
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ISA/US		 Gary L. Junz	



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Category *	Citation of Document, with indication, where appropriate, of the relevant passages	Relevant to Claim No
Y	Proc. Natl. Acad. Sci. Vol. 86, issued September 1989, KULKA ET AL, "Site specificity of the inhibitory effects of oligo (nucleoside methylphosphonate)s complementary to the acceptor splice junction of herpes simplex virus type 1 immediate early mRNA 4" See pages 6868-6872.	1-26
Y	Journal of Virology, Vol. 61, No. 8, issued August 1987, BLAIR ET AL, "Herpes Simplex Virus Stimulatory Protein mRNA Leader Contains Sequence Elements Which Increase Both Virus-Induced Transcription and mRNA Stability" See pages 2499-2508.	1-26
Y	Journal of Molecular Biology, Vol. 181, issued 1985, MCGEOCH ET AL "Sequence Determination and Genetic Content of the Short Unique Region in the Genome of Herpes Short Unique Region in the Genome of Herpes Simplex Virus Type 1" See pages 1-13.	1-26
Y	Journal of General Virology, Vol. 69, issued 1988, PERRY ET AL, "The DNA Sequences of the Long Repeat Region and Adjoining Parts of the Long Unique Region in the Genome of Herpes Simplex Virus Type 1" See pages 2831-2846.	
Y	Proc. Natl. Acad. Sci., Vol. 83, issued May 1986, SMITH ET AL, "Antiviral effect of an oligo (nucleoside methylphosphonate) complementary to the splice junction of herpes simplex virus type 1 immediate early premRNAs 4 and 5" See pages 2787-2791.	1-26
Y	Journal of General Virology, Vol. 69, issued 1988, MCGEOCH ET AL, "The Complete DNA Sequence of the Long Unique Region in the Genome of Herpes Simplex Virus Type 1" See pages 1531-1574.	1-26

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